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S	A	A	A	L	T	L	A	R	P	P	A	A	R	L	A	L	L	M	A	P	P	A	A	R	L	A	L	L	11
TCC	GCC	GCG	GCG	CTC	ACG	CTG	GCG	GCC	CGG	CCC	GCG	CCT	AGC	CCC	GGC	CTC	GGC	CCC	GCC	CGC	CGC	CTG	66						
P	E	C	F	T	A	N	G	A	D	Y	R	G	T	Q	N	W	T	A	L	51									
CCC	GAG	TGT	TTC	ACA	GCC	AAT	GGT	GCG	GAT	TAT	AGG	GGA	ACA	CAG	AAC	TGG	ACA	GCA	GCA	CTA	186								
Q	G	G	K	P	C	L	F	W	N	E	T	F	Q	H	P	Y	N	T	L	51									
CAA	GGC	GGG	AAG	CCA	TGT	CTG	TTT	TGG	AAC	GAG	ACT	TTC	CAG	CAT	CCA	TAC	AAC	ACT	CTG	1 / 95									
K	Y	P	N	G	E	G	G	L	G	E	H	N	Y	C	R	N	P	D	G	71									
AAA	TAC	CCC	AAC	GGG	GAG	GGG	GGC	CTG	GGT	GAG	CAC	AAC	TAT	TGC	AGA	AAT	CCA	GAT	GGA	246									
D	V	S	P	W	C	Y	V	A	E	H	E	D	G	V	Y	W	K	Y	C	91									
GAC	GTG	AGC	CCC	TGG	TGC	TAT	GTG	GCA	GAG	CAC	GAG	GAT	GGT	GTC	TAC	TGG	AAG	TAC	TGT	306									
E	I	P	A	C	Q	M	P	G	N	L	G	C	Y	K	D	H	G	N	P	111									
GAG	ATA	CCT	GCT	TGC	CAG	ATG	CCT	GGA	AAC	CTT	GGC	TGC	TAC	AAG	GAT	CAT	GGA	AAC	CCA	366									
P	P	L	T	G	T	S	K	T	S	N	K	L	T	I	Q	T	C	I	S	131									
CCT	CCT	CTA	ACT	GGC	ACC	AGT	AAA	ACG	TCC	AAA	ACG	CTC	ACC	ATA	CAA	ACT	TGC	ATC	AGT	426									
F	C	R	S	Q	R	F	K	F	A	G	M	E	S	G	Y	A	C	F	C	171									
TTT	TGT	CGG	AGT	CAG	AGG	TTC	AAG	TTT	GCT	GGG	ATG	GAG	TCA	GGC	TAT	GCT	TGC	TTC	TGT	546									

Fig. 1A



G	N	N	P	D	Y	W	K	Y	G	E	A	A	S	T	E	C	N	S	V	
GGAA	AAC	AAT	CCT	GAT	TAC	TGG	AAG	TAC	GGG	GAG	GCA	GCC	AGT	ACC	GAA	TGC	AAC	AGC	GTC	
191																				
C	F	G	D	H	T	Q	P	C	G	D	G	R	I	I	L	F	D	T	211	
TGC	TTC	GGG	GAT	CAC	ACC	CAA	CCC	TGT	GGT	GGC	GAT	GGC	AGG	ATC	ATC	CTC	TTT	GAT	ACT	666
L	V	G	A	C	G	G	N	Y	S	A	M	S	S	V	V	Y	S	P	D	231
CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA	GCC	ATG	TCT	TCT	GTG	GTC	TAT	TCC	CCT	GAC	726
F	P	D	T	Y	A	T	G	R	V	C	Y	W	T	I	R	V	P	G	A	251
TTC	CCC	GAC	ACC	TAT	GCC	ACG	GGG	AGG	GTC	TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCG	GGG	GCC	786
S	H	I	H	F	S	F	P	L	F	D	I	R	D	S	A	D	M	V	E	271
TCC	CAC	ATC	CAC	TTC	AGC	TTC	CCC	CTA	TTT	GAC	ATC	AGG	GAC	TCG	GCG	GAC	ATG	GTG	GAG	846
L	L	D	G	Y	T	H	R	V	L	A	R	F	H	G	R	S	R	P	P	291
CTT	CTG	GAT	GGC	TAC	ACC	CAC	CGT	GTC	CTA	GCC	CGC	TTC	CAC	GGG	AGG	AGC	CGC	CCA	CCT	906
L	S	F	N	V	S	L	D	F	V	I	L	Y	F	F	S	D	R	I	N	311
CTG	TCC	TTC	AAC	GTC	TCT	CTG	GAC	TTC	GTC	ATC	TTG	TAT	TTC	TTC	TCT	GAT	CGC	ATC	AAT	966
Q	A	Q	G	F	A	V	L	Y	Q	A	V	K	E	E	L	P	Q	E	R	331
CAG	GCC	CAG	GGA	TTT	GCT	GTT	TTA	TAC	CAA	GCC	GTC	AAG	GAA	CTG	CCA	CAG	GAG	AGG	1026	
																			2 / 95	

Fig. 1B



P A V N Q T V A E V I T E Q A N L S V S 351
 CCC GCT GTC AAC CAG ACG GTG GCC GAG GTG ATC ACG GAG CAG GCC AAC CTC AGT GTC AGC AGC 1086

 A A R S S K V L Y V I T T S P S H P P Q 371
 GCT GCC CGG TCC TCC AAA GTC CTC TAT GTC ATC ACC ACC AGC CCC AGC CAC CCA CCT CAG CAG 1146

 T V P G S N S W A P P M G A G S H R V E 391
 ACT GTC CCA GGT AGC ATT TCC TGG GCG CCA CCC ATG GGG GCT GGA AGC CAC AGA GTT GAA 1206

 G W T V Y G L A T L L I L T V T A I V A 411
 GGA TGG ACA GTC TAT GGT CTG GCA ACT CTC CTC ATC ATC GTC ACA GTC ACA GCC ATT GTA GCA 1266

 K I L H V T F K S H R V P A S G D L R 431
 AAG ATA CTT CTG CAC GTC ACA TTC AAA TCC CAT CGT GTT CCT GCT TCA GGG GAC CTT AGG 1326

 D C H Q P G T S G E I W S I F Y K P S T 451
 GAT TGT CAT CAA CCA CCA GGG ACT TCG GGG GAA ATC TGG AGC ATT TTT TAC AAG CCT TCC ACT 1386

 S I S I F K K L K G Q S Q Q D D R N P 471
 TCA ATT TCC ATC TTT AAG AAG AAA CTC AAG GGT CAG AGT CAA CAA GAT GAC CGC AAT CCC 1446

 L V S D * 476
 CTT GTG AGT GAC TAA 1461

Fig. 1C



AAACCCCACTGTGCCCTAGGACTTGGAGGCTTCTTGAGGCTCAAGGCTGCCGTGGTCAACCTCCTGTGGTTCTCTC
TGACAGACTCTCCCTCTCTGGCTCTGGCTCTGGAAACCCCTCCTACAGACTTAGGAAGAGGCACCT 1540
GCTGCCAGGGCAGGCAGAGCCTGGATTCCCTGGCT 1620
1657

Fig. 1D

GTCGACCCACGGTCCGGCGCTCCGGTGCCTGCCCTCTGCCGGGGTCCCCGACTGACGGCC 79

M A P P A R L A L S A A A L T I A 19
C ATG GCG CCG CCC GCC CGT CTC GCG CTG CTC TCC GCC GCT GCG CTC ACT CTG GCG 137 4 / 95

A R P A P G P R S G P E C F T A N G A D 39
GCC CCC GCG CCC GGT CCC CGC TCC GGC CCC GAG TGC TTC ACA GCC AAC GGT GCA GAT 197

Y R G T Q S W T A L Q G G K P C L F W N 59
TAC AGG GGA ACA CAG AGC TGG ACA GCG CTG CAA GGT GGG AAG CCA TGT CTG TTC TGG AAC 257

E T F Q H P Y N T L K Y P N G E G G L G 79
GAG ACT TTC CAG CAT CCG TAC AAC ACG CTG AAG TAC CCC AAC GGG GAA GGA CTG GGC 317

E H N Y C R N P D G D V S P W C Y V A E 99
GAG CAC AAT TAT TGC AGA AAT CCA GAT GGA GAC GTG AGC CCT TGG TAC GTG GCC GAG 377

Fig. 1E



H	E	D	G	V	Y	W	K	Y	C	E	I	P	A	C	Q	M	P	G	N
CAT	GAG	GAC	GGA	GTC	TAC	TGG	AAG	TAC	TGT	GAA	ATT	CCT	GCC	TGC	CAG	ATG	CCT	GGA	AAC
L	G	C	Y	K	D	H	G	N	P	P	P	L	T	G	T	S	K	T	S
CTT	GGC	TGC	TAC	AAG	GAT	CAT	GGA	AAC	CCA	CCT	CCT	CTC	ACG	GGC	ACC	AGT	AAA	ACC	TCT
N	K	L	T	I	Q	T	C	I	S	F	C	R	S	Q	R	F	K	F	A
AAC	AAG	CTC	ACC	ATA	CAA	ACC	TGT	ATC	AGC	TTC	TGT	CGG	AGT	CAG	AGA	TTC	AAG	TTT	GCT
G	M	E	S	G	Y	A	C	F	C	G	N	N	P	D	Y	W	K	H	G
GGG	ATG	GAG	TCA	GGC	TAT	GCC	TGC	TTC	TGT	GGG	AAC	AAT	CCT	GAC	TAC	TGG	AAG	CAC	GGG
E	A	A	S	T	E	C	N	S	V	C	F	G	D	H	T	Q	P	C	G
GAG	GCG	GCC	AGC	ACC	GAG	TGC	AAT	AGT	GTC	TGC	TTC	GGG	GAC	CAC	ACG	CAG	CCC	TGC	GGT
G	D	G	R	I	I	L	F	D	T	L	V	G	A	C	G	G	N	Y	S
GGG	GAC	GGC	AGG	ATT	ATC	CTC	TTT	GAC	ACT	CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA
A	M	A	A	V	V	Y	S	P	D	F	P	D	T	Y	A	T	G	R	V
GCC	ATG	GCA	GCC	GTG	GTG	TAC	TCC	CCT	GAC	TTC	CCT	GAC	ACC	TAC	GCC	ACT	GGC	AGA	GTC
C	Y	W	T	I	R	V	P	G	A	S	R	I	H	F	N	F	T	L	F
TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCA	GGA	GCC	TCT	CGC	ATC	CAT	TTC	AAC	TTC	ACC	CTG	TTT
D	I	R	D	S	A	D	M	V	E	L	L	D	G	Y	T	H	R	V	L
GAT	ATC	AGG	GAC	TCT	GCA	GAC	ATG	GTG	GAG	CTG	CTG	GAC	GGC	TAC	ACC	CAC	CGC	GTC	CTG

Fig.1F



V	R	L	S	G	R	S	R	P	P	L	S	F	N	V	S	L	D	F	V	
GTC	CGG	CTC	AGT	GGG	AGG	AGC	CGC	CCG	CCT	CTG	TCT	AAT	GTC	TCT	CTG	GAT	TTT	GTC	299	
I	L	Y	F	F	S	D	R	I	N	Q	A	Q	G	F	A	V	L	Y	Q	977
ATT	TTG	TAT	TTC	TTC	TCT	GAT	CGC	ATC	AAT	CAG	GCC	CAG	GGA	TTT	GCT	GTG	TAC	CAA	1037	
A	T	K	E	E	P	P	Q	E	R	P	A	V	N	Q	T	L	A	E	V	319
GCC	ACC	AAG	GAG	GAA	CCG	CCA	CAG	GAG	AGA	CCT	GCT	GTC	AAC	CAG	ACC	CTG	GCA	GAG	GTG	1097
I	T	E	Q	A	N	L	S	V	S	A	A	H	S	S	K	V	L	Y	V	359
ATC	ACC	GAG	CAA	GCC	AAC	CTC	AGT	GTC	AGC	GCT	GCC	CAC	TCC	TCC	AAA	GTC	CTC	TAT	GTC	1157
I	T	P	S	P	S	H	P	P	Q	T	A	Q	V	A	I	P	G	H	R	379
ATC	ACC	CCC	AGC	CCC	AGC	CAC	CCT	CCG	CAG	ACT	GCC	CAG	GTA	GCC	ATT	CCT	GGG	CAC	CGT	1217
Q	L	G	P	T	A	T	E	W	K	D	G	L	C	T	A	W	R	P	S	379
CAG	TG	GGG	CCA	ACA	GCC	ACA	GAG	TGG	AAG	GAT	GGA	CTG	TGT	ACG	GCC	TGG	CGA	CCC	TCC	1277
S	S	S	Q	S	Q	Q	L	S	Q	R	F	F	C	M	S	H	L	N	L	419
TCA	TCC	TCA	CAG	TCA	CAG	CAG	TTG	TCG	CAA	AGA	TTC	TTC	TGC	ATG	TCA	CAT	TTA	AAT	CTC	1337
I	E	S	L	H	Q	E	T	L	G	T	V	V	S	L	G	L	L	E	I	439
ATC	GAG	TCC	CTG	CAT	CAG	GAG	ACC	TTA	GGG	ACT	GTC	GTC	AGC	CTG	GGG	CTT	CTG	GAG	ATA	1397
S	G	P	F	S	M	N	L	P	L	Q	S	P	S	L	R	R	S	S	R	459
TCT	GGA	CCA	TTT	TCT	ATG	AAC	CTT	CCA	CTA	CAA	TCT	TCA	AGA	AGA	AGC	TCA	AGG	1457		

Fig.1G

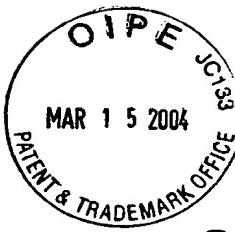


V R N K M T A I P S *
 GTC AGA GTC AAC AAG ATG ACC GCA ATC CCC TCG TGA

471
 1493

GTGACTGAAGCCCCACGCCCTGCATGAGAGGCTCCGCTCCAAGCTTGGCTCCCCTGAGTTCTCCTGATGAGTTC 1572
 CCTGCCCTTCCATTACCACCATCTCTTGGAGCACCCCTGCTTTAGAGGCAGCCCAGGCTGGATCCTCCATCACAT 1651
 GTACCCAGCCTGGCTCTGCTGGGATGGTAAGACAGGCCAGGCTGACAGGACACAGCTGGACCTCCAGAAAGA 1730
 CTCTTGGGGTGGTGGGGAGGTATAGTGTAGGGATGAGTTTCTTGCTTCTGCTTCTGCTGTTCTGCTGTTCTGCT 1809
 CCCTGTCTTACAGTTGCAATTAGAGCCAGACTGAAGAACACTGTAGGCTTGGAGCTTTCTGCTGCCAACTACCATG 1888
 GTGGCATTGGGCCCTAGAGGCCAGGCCCCAGGAGGCCACACCAGATGTCATCTTCTAGAGGGTTCTTTAGACCCACTG 1967
 AGTCCGGAGGGACTGAGGCCAGGAGGCCACACCAGATGTCATCTTCTAGAGGGTTCTTTAGACCCACTGACCAAATGG 2046
 GGCAAGGCCTGAGGATTGGGATTTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 2125
 TAGCCCCCTCAAGTAGTTGCCAATCCTGTGAATCAGAATTAGCCTAGGCTGTGTCTAGGCCAAGCCTGTAGCCCTAG 2204
 AGCTGGGGCTGTAGCCTAGAGCTGGGCTGTAGCCTAGAGCTGGGCTGTAGCCTAGAGCTGGGCTGTAGCAGAGCTGG 2283
 TGGGGCTGTAGCACAGAGCTGGGCTGTAGCCTAGAGCTGGGCTGTAGCAGAGCTGGGCTGTAGCACAGAGCTGG 2362
 GGCTGTAGCCTAGAGCTGGGCTGTAGCACAGAGCTGGGCTGTAGCAGAGCTGGGCTGTAGCACAGAGCTGGGCTGT 2441
 GACCCTAGGTTCTATCCCAAGCACTATCAGAAGGGTGGGAGAGAAAAGACTGCACCATAGCATGGGGCAGCATCTGTGG 2520
 TTCCCTACGTGAGGTGTCAATTAAAGCAGATCAAAACTACCCGGAGTTCAGTGGGGCTAGAGCTGGGAGAGGAGGGCAG 2599
 AGAGTAGGGAGTAAGGGCTCTGGCTCATTTAAAGCAGATCAAAACTACCCGGAGTGGGGAGAGGAGGGCAG 2678
 GATCCTCCAGAAAAGCTGCAAGATTGAGAGACCCAGCTGCAGTGGGAGAGGAGGGCAGTGGTAGACCTTGGTCAC 2757
 CTGCAGTGGAAAGTGGCCTTGTCAAGCAGCAGCTGTGGCCCTGAAGGTAGACCTTGGTCACCTCTGGCAGCCCTTG 2836
 GCCTCTGCTCTGGTACCCCTGGCTACCTGGCAACCCATGCTAACCTTCCCCAGTCTCAGTCAGTCACTGCCATGAGGCCTC 2915
 TCCTCTAGCTGCTGGTCCCCAGGACTGTGGGATCAGGGAGGGCAGGAGTCACTGAGTCAGTGGCTCAGCTGGGAGGCC 2994
 TGACCTGAGCTGATGAGTCACCAAGAGACACCAGAGCTACAGTGGCTGCTGGCTCAGCTGGGAGGCC 3073
 TACAGGGGTACTTAAGCTAGGGGTCACTCATCTCATTTGATCTGAGGCTACAGGAAAGGCTACAGGAAAGACAGGCC 3152
 CACTACATAAGAAGACCACCTGAGGAGCAGGTTCCACTAGCAGCTGTCCATAGCAGCTGTGGCTTGCAGGAGACTC 3231

Fig.1H



CCCTGAGACCAAGTGTGAGTCACAGAGTCCATGTGCCATTAGGATAATGGGTTCTTAACCAGGGAAAGGGCTC
 ATAGCAGGCCAGGACATTTTCAGCTCAGAGCACTGGCCACTTCAAGCCACCTCACCTGGCTTCTAAGCCACCC
 ATCTCGGACACAGGAAGCAAGCCCCAGTGTGGCAGCTGCGGCTCAGCATTGGTGTCCCCAGGAAGGGGGATG
 TGCCCAACGGCTCCTTGTGGCCTGGCACAGCCCACACTGCAGGGCACACTTCTGGGGGACTCTGGGGTAGGGACAC
 ATAAGGAAAACCTAACCCACCTCCAACAACAGCAGGGACAGTGGGAAGGGCTGTAAATCACCCAGGGCAGACCTC
 CAGAAATGACAGGCACAGTGTAGAACCTGTAGGCAAGTCACAGGGCCTTGGCTGGTAACACCCCTGGCTG
 GAGCATAGGGTAAGCCGAGGGAGAACAGCAGGGCTCAGAGACATCAGCTAAACATAGGTGCCCTATGTC
 TCCTGTCACACTGCTTACAAGCAGAGCTAGGAAGAGGTCTGGACTTCTAAATGTGGCTCTGGCCAGCCC
 GGGCTGCCTAAAGTGAGCAAGGAAACAGAGCTCTGGGGTACAGCTGGCCAGGGCATGGGATGTGGCT
 AAAGGCTCTTGAAGATCAAAGCTCTGGGGTACAGCTGGCCAGGGACAGACTGACTACACTTGACCT
 GTGCCACCCACGGCTCACTGTCACTGGCTCCTCATCCGGCTGGCCTGACACTATCA
 GAGGCTCGGCCGGCTGTGGCCAGGGACAGACTGACTACACTTGACCTTCAAGAGCACTTGAAGTGG
 CTCTGTCAGCCCTCTGCAGGGGCACACAAGTCTCCGGCAAGTCCACAAAGCTCCATGGTTCCCT
 GTGGGAGTGTCCCTGTTGATGTCTGAGGTCTGGCTCTGGCTCTGGGAAACTGCTAACCTCCG
 GTCTCTGTTACTGTCCCTCTTACCTCCAGGTCACTTAGCTAGCTGGCTCTGGGAGTGGGGATGCT
 GGCTGCACCCACCCCTGGCTGGCCAAACAGAACCTGGGGCCTCACACGGGCTCCTGGCTGGAGCTGAGC
 ACACTGGCCAGGGCTGAGTGGGGAGTCTCTCTTAGAGGGAGTGGGGAGTGGCTGGGGATGCT
 AGATCCAGGGAGGGCTGCCATCCCCGCCACCTCATAGCAGCAAGACCTCCATTCCAATTC
 GGATATGACTTGGACAACAAGGCTTATTGTAAATATGCAACTTGTAGAATAAGATA
 TGTATTAAATATAAAATGAAGTGTGACACACTGTATAACATTAAATATATTTAGGATTGTT
 AATGGAAATGTGATGGTACTTAACCTTACAAAGAGAAAATGTTTACTGTTGAAGAAAATA
 TTGGTAGAAAAAAAGGGGGCGC
 3310
 3389
 3468
 3547
 3626
 3705
 3784
 3863
 3942
 4021
 4100
 4179
 4258
 4337
 4416
 4495
 4574
 4653
 4732
 4811
 4890
 4928

Fig.11



Hum.	MAPPALARLLSAAALTЛАARPAPSPGLGPPECFTANGADYRGQTQNWTALQGGKPCLFWNETFQHPYNT	10	20	30	40	50	60	70
Mur.	MAPPALARLLSAAALTЛАARPAPGPR--SGPECFTANGADYRGQTQSWTALQGGKPCLFWNETFQHPYNT	10	20	30	40	50	60	
Hum.	LKYPNCEGGLGEHNYCRNPDGDVSPWCYVAEHEDGVYWMKYCEIPACQMPGNLGCYKDHNPPPLTGTTSKT	80	90	100	110	120	130	140
Mur.	LKYPNCEGGLGEHNYCRNPDGDVSPWCYVAEHEDGVYWMKYCEIPACQMPGNLGCYKDHNPPPLTGTTSKT	70	80	90	100	110	120	
Hum.	SNKLTIQTCISFCRSQRKEAGMESGYACFCGNNPDYWKYGEAASTE CNSVCFGDHTQPCGGDGRILFD	150	160	170	180	190	200	210
Mur.	SNKLTIQTCISFCRSQRKEAGMESGYACFCGNNPDYWKHGEAASTE CNSVCFGDHTQPCGGDGRILFD	140	150	160	170	180	190	200
Hum.	TLVGACGGNYSAMSSVVYSPDFPDTYATGRVCYWTIRPGASHIHFSFPLFDIIRDSADMVELLDGYTHRV	220	230	240	250	260	270	280
Mur.	TLVGACGGNYSAMAAVYSPDFPDTYATGRVCYWTIRPGASRIHENFTLFDIIRDSADMVELLDGYTHRV	210	220	230	240	250	260	270

Fig.1J



10 / 95

Hum.	LARFHGRSRPPLSFNVSLDFVILYFFSDRINQAAQGFAVILYQAVKEELPQERPAVNQTVAEVITEQANLSV	290	300	310	320	330	340	350
Mur.	LVRLSGRSRPPPLSFNVSLDFVILYFFSDRINQAAQGFAVILYQATKEEPPQERPAVNQTLAEVITEQANLSV	280	290	300	310	320	330	340
Hum.	SAARSSKVLYVITTSPPSHPPOTVPGNSNWWAPPMGAGSHRVEGWTIVYGLATLLILTVTAIVAKILLHVTEK	360	370	380	390	400	410	420
Mur.	SAAHSSKVLYVITTPSPSPHPPQTAQVAIPGHRLGPTA---TEWKD-GLCTAWRPSSSSQQQLSQRFFCM	350	360	370	380	390	400	410
Hum.	SHRVPAASGDLRDCHQPGTSGEIWSIFYKPSTSISIFKKKLKGQSQ-QDDRNPLVSD	430	440	450	460	470		
Mur.	SHLNLLIESLHQETLGLTVVSIGLLEISGPFSMNLPLQSSPSLRRSSSRVNVNKMIAIFS	420	430	440	450	460		470

Fig.1K



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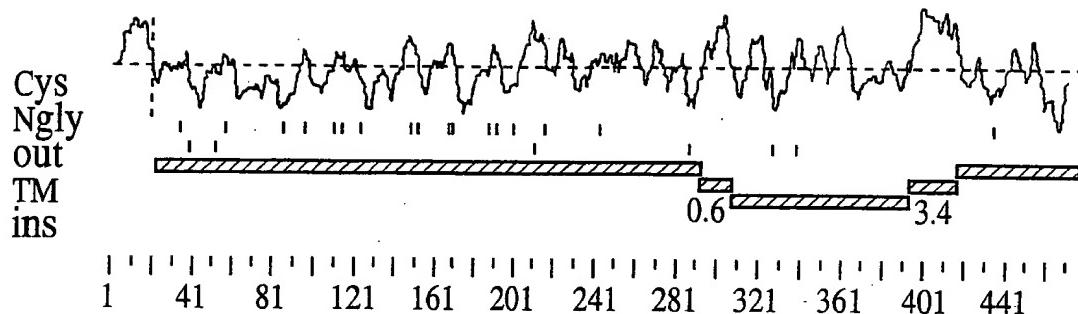


Fig. 1L

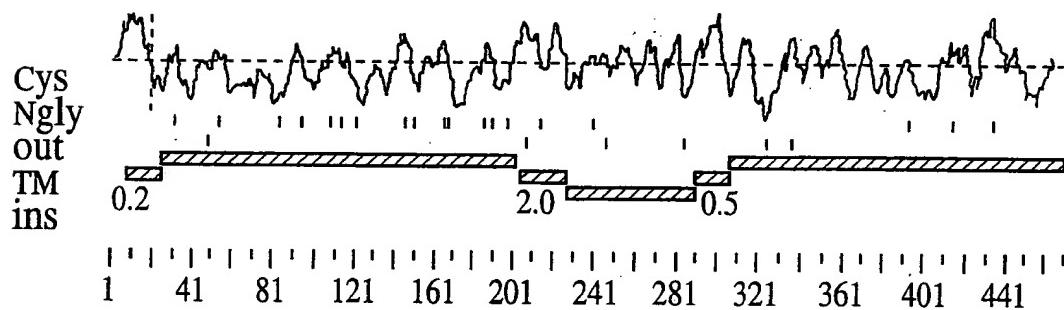


Fig. 1M



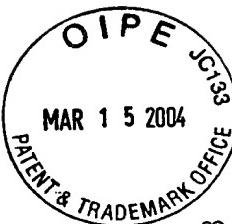
	M	M	L	P	Q	N	S	W	H	I	D	F	G	13						
	GGGGCGCTCGCGATCTAGAAGTAGTA	ATG	ATG	CTG	CCT	CAA	AAC	TCG	TGG	CAT	ATT	GAT	TTT	GGA	66					
R	C	C	H	Q	N	L	F	S	A	V	T	C	I	L	33					
AGA	TGC	TGC	TGT	CAT	CAG	AAC	CTT	TTC	TCT	GCT	GTG	GTA	ACT	TGC	ATC	CTG	CTC	CTG	AAT	126
S	C	F	L	I	S	S	F	N	G	T	D	L	E	L	R	L	V	N	G	53
TCC	TGC	TTT	CTC	ATC	AGC	AGT	TTT	AAT	GGA	ACA	GAT	TTG	GAG	TTG	AGG	CTG	GTC	AAT	GGA	186
D	G	P	C	S	G	T	V	E	V	K	F	Q	G	Q	W	G	T	V	C	73
GAC	GGT	CCC	TGC	TCT	GGG	ACA	GTG	GAG	GTG	AAA	TTC	CAG	GGA	CAG	TGG	GGG	ACT	GTG	TGT	246
D	D	G	W	N	T	T	A	S	T	V	V	C	K	Q	L	G	C	P	F	93
GAT	GAT	GGG	TGG	AAC	ACT	ACT	GCC	TCA	ACT	GTC	GTG	TGC	AAA	CAG	CTT	GGA	TGT	CCA	TTT	306
S	F	A	M	F	R	F	G	Q	A	V	T	R	H	G	K	I	W	L	D	113
TCT	TTC	GCC	ATG	TTT	CGT	TTT	GGA	CAA	GCC	GTG	ACT	AGA	CAT	GGA	AAA	ATT	TGG	CTT	GAT	366
D	V	S	C	Y	G	N	E	S	A	L	W	E	C	Q	H	R	E	W	G	133
GAT	GTT	TCC	TGT	TAT	GGA	AAT	GAG	TCA	GCT	CTC	TGG	GAA	TGT	CAA	CAC	CGG	GAA	TGG	GGA	426
S	H	N	C	Y	H	G	E	D	V	G	V	N	C	Y	G	E	A	N	L	153
AGC	CAT	AAC	TGT	TAT	CAT	GGA	GAA	GAT	GTT	GGT	AAC	TGT	TAT	GGT	GAA	GCC	AAT	CTG	486	

Fig. 2A



G	L	R	L	V	D	G	N	N	S	C	S	G	R	V	E	V	K	F	Q
GGT	TTC	AGG	CTA	GTG	GAT	GGA	AAC	AAC	TCC	TGT	TCA	GGG	AGA	GTG	GAG	GTG	AAA	TTC	CAA
E	R	W	G	T	I	C	D	D	G	W	N	L	N	T	A	A	V	V	C
GAA	AGG	TGG	GGG	ACT	ATA	TGT	GAT	GGA	GGG	TGG	AAC	TTG	AAT	ACT	GCT	GCC	GTG	GTG	TGC
R	Q	L	G	C	P	S	S	F	I	S	S	G	V	V	N	S	P	A	V
AGG	CAA	CTA	GGA	TGT	CCA	TCT	TCT	TTT	ATT	TCT	TCT	GGA	GTT	GTT	AAT	AGC	CCT	GCT	GTA
L	R	P	I	W	L	D	D	I	L	C	Q	G	N	E	L	A	L	W	N
TTG	CGC	CCC	ATT	TGG	CTG	GAT	GAC	ATT	TTA	TGC	CAG	GGG	AAT	GAG	TTG	GCA	CTC	TGG	AAT
C	R	H	R	G	W	G	N	H	D	C	S	H	N	E	D	V	T	L	T
TGC	AGA	CAT	CGT	GGA	TGG	GGA	AAT	CAT	GAC	TGC	AGT	CAC	AAT	GAG	GAT	GTC	ACA	TTA	ACT
C	Y	D	S	S	D	L	E	L	R	L	V	G	G	T	N	R	C	M	G
TGT	TAT	GAT	AGT	AGT	GAT	CTT	GAA	CTA	AGG	CTT	GTA	GGT	GGA	ACT	AAC	CGC	TGT	ATG	GGG
R	V	E	L	K	I	Q	G	R	W	G	T	V	C	H	H	K	W	N	N
AGA	GTA	GAG	CTG	AAA	ATC	CAA	GGA	AGG	TGG	GGG	ACC	GTA	TGC	CAC	CAT	AAG	TGG	AAC	AAT
A	A	A	D	V	V	C	K	Q	L	G	C	G	T	A	L	H	F	A	G
GCT	GCA	GCT	GAT	GTC	GTC	GTA	TGC	AAG	CAG	TTG	GGA	TGT	GGA	ACC	GCA	CTT	CAC	TTC	GCT
L	P	H	L	Q	S	G	S	D	V	V	W	L	D	G	V	S	C	S	G
TTG	CCT	CAT	TTG	CAG	TCA	GGG	TCT	GAT	GTT	GTA	TGG	CTT	GAT	GGT	GTC	TCC	TGC	TCC	GGT

Fig. 2B



N	E	S	F	L	W	D	C	R	H	S	G	T	V	N	F	D	C	L	H	353	
AAT	GAA	TCT	TTT	CTT	TGG	GAC	TGC	AGA	CAT	TCC	GGA	ACC	GTC	AAT	TTT	GAC	TGT	CTT	GCA	GAT	1086
Q	N	D	V	S	V	I	C	S	D	G	A	D	L	E	L	R	L	A	D	373	
CAA	AAC	GAT	GTG	TCT	GTG	ATC	TGC	TCA	GAT	GGA	GCA	GAT	TTG	GAA	CTG	CGA	CTA	GCA	GAT	1146	
G	S	N	N	C	S	G	R	V	E	V	R	I	H	E	Q	W	W	T	I	393	
GGA	AGT	AAC	AAT	TGT	TCA	GGG	AGA	GTA	GAG	GTG	AGA	ATT	CAT	GAA	CAG	TGG	TGG	ACA	ATA	1206	
C	D	Q	N	W	K	N	E	Q	A	L	V	V	C	K	Q	L	G	C	P	413	
TGT	GAC	CAG	AAC	TGG	AAG	AAT	GAA	CAA	GCC	CTT	GTG	GTG	TGT	TGT	AAG	CAG	CTA	GGA	TGT	CCG	1266
F	S	V	F	G	S	R	R	A	K	P	S	N	E	A	R	D	I	W	I	433	
TTC	AGC	GTC	TTT	GGC	AGT	CGT	CGT	GCT	AAA	CCT	AGT	AAT	GAA	GCT	AGA	GAC	ATT	TGG	ATA	1326	
N	S	I	S	C	T	G	N	E	S	A	L	W	D	C	T	Y	D	G	K	453	
AAC	AGC	ATA	TCT	TGC	ACT	GGG	AAT	GAG	TCA	GCT	CTC	TGG	GAC	TGC	ACA	TAT	GAT	GGA	AAA	1386	
A	K	R	T	C	F	R	R	S	D	A	G	V	I	C	S	D	K	A	D	473	
GCA	AAG	CGA	ACA	TGC	TTC	CGA	AGA	TCA	GAT	GCT	GGA	GTA	ATT	TGT	TCT	GAT	AAG	GCA	GAT	1446	
L	D	L	R	L	V	G	A	H	S	P	C	Y	G	R	L	E	V	K	Y	493	
CTG	GAC	CTA	AGG	CTT	GTC	GGG	GCT	CAT	AGC	CCC	TGT	TAT	GGG	AGA	TTG	GAG	GTG	AAA	TAC	1506	
Q	G	E	W	G	T	V	C	H	D	R	W	S	T	R	N	A	A	V	V	513	
CAA	GGA	GAG	TGG	GGG	ACT	GTG	TGT	CAT	GAC	AGA	TGG	AGC	ACA	AGG	AAT	GCA	GCT	GTT	GTG	1566	

Fig. 2C



C	K	Q	L	G	C	G	K	P	M	H	V	F	G	M	T	Y	F	K	E	
TGT	AAA	CAA	TTG	GGA	TGT	GGA	AAG	CCT	ATG	CAT	GTG	TTT	GGT	ATG	ACC	TAT	TTT	AAA	GAA	1626
A	S	G	P	I	W	L	D	D	V	S	C	I	G	N	E	S	N	I	W	553
GCA	TCA	GGA	CCT	ATT	TGG	CTG	GAT	GAC	GTT	TCT	TGC	ATT	GGA	AAT	GAG	TCA	AAT	ATC	TGG	1686
D	C	E	H	S	G	W	G	K	H	N	C	V	H	R	E	D	V	I	V	573
GAC	TGT	GAA	CAC	AGT	GGA	TGG	GGA	AAG	CAT	AAT	TGT	GTA	CAC	AGA	GAG	GAT	GTG	ATT	GTA	1746
T	C	S	G	D	A	T	W	G	L	R	L	V	G	G	S	N	R	C	S	593
ACC	TGC	TCA	GGT	GAT	GCA	ACA	TGG	GGC	CTG	AGG	CTG	GTG	GGC	GGC	AGC	AAC	CGC	TGC	TCG	1806
G	R	L	E	V	Y	F	Q	G	R	W	G	T	V	C	D	D	G	W	N	613
GGA	AGA	CTG	GAG	GTG	TAC	TTT	CAA	GGA	CGG	TGG	GGC	ACA	GTG	TGT	GAT	GAC	GGC	TGG	AAC	1866
S	K	A	A	A	V	V	C	S	Q	L	D	C	P	S	S	I	I	G	M	633
AGT	AAA	GCT	GCA	GCT	GTG	GTG	TGT	AGC	CAG	CTG	GAC	TGC	TCA	TCT	TCT	ATC	ATT	GGC	ATG	1926
G	L	G	N	A	S	T	G	Y	G	K	I	W	L	D	D	V	S	C	D	653
GGT	CTG	GGA	AAC	GCT	TCT	ACA	GGA	TAT	GGA	AAA	ATT	TGG	C'TC	GAT	GAT	GTT	TCC	TGT	GAT	1986
G	D	E	S	D	L	W	S	C	R	N	S	G	W	G	N	N	D	C	S	673
GGA	GAT	GAG	TCA	GAT	CTC	TGG	TCA	TGC	AGG	AAC	AGT	GGG	TGG	GGA	AAT	AAT	GAC	TGC	AGT	2046
H	S	E	D	V	G	V	I	C	S	D	A	S	D	M	E	L	R	L	V	693
CAC	AGT	GAA	GAT	GTT	GGA	GTG	ATC	TGT	TCT	GAT	GCA	TCG	GAT	ATG	GAG	CTG	AGG	CTT	GTG	2106

Fig. 2D



G	G	S	S	R	C	A	G	K	V	E	V	N	V	Q	G	A	V	G	I	713
GGT	GGA	AGC	AGC	AGG	TGT	GCT	GGA	AAA	GTT	GAG	GTC	AAT	GTC	CAG	GGT	GCC	GTG	GGA	ATT	2166
L	C	A	N	G	W	G	M	N	I	A	E	V	V	C	R	Q	L	E	C	733
CTG	TGT	GCT	AAT	GGC	TGG	GGA	ATG	AAC	ATT	GCT	GAA	GTT	GTT	TGC	AGG	CAA	CTT	GAA	TGT	2226
G	S	A	I	R	V	S	R	E	P	H	F	T	E	R	T	L	H	I	L	753
GGG	TCT	GCA	ATC	AGG	GTC	TCC	AGA	GAG	CCT	CAT	TTC	ACA	GAA	AGA	ACA	TTA	CAC	ATC	TTA	2286
M	S	N	S	G	C	T	G	G	E	A	S	L	W	D	C	I	R	W	E	773
ATG	TCG	AAT	TCT	GGC	TGC	ACT	GGA	GGG	GAA	GCC	TCT	CTC	TGG	GAT	TGT	ATA	CGA	TGG	GAG	2346
W	K	Q	T	A	C	H	L	N	M	E	A	S	L	I	C	S	A	H	R	793
TGG	AAA	CAG	ACT	GCG	TGT	CAT	TTA	AAT	ATG	GAA	GCA	AGT	TTG	ATC	TGC	TCA	GCC	CAC	AGG	2406
Q	P	R	L	V	G	A	D	M	P	C	S	G	R	V	E	V	K	H	A	813
CAG	CCC	AGG	CTG	GTT	GGA	GCT	GAT	ATG	CCC	TGC	TCT	GGA	CGT	GTT	GAA	GTG	AAA	CAT	GCA	2466
D	T	W	R	S	V	C	D	S	D	F	S	L	H	A	A	N	V	L	C	833
GAC	ACA	TGG	CGC	TCT	GTC	TGT	GAT	TCT	GAT	TTC	TCT	CTT	CAT	GCT	GCC	AAT	GTG	CTG	TGC	2526
R	E	L	N	C	G	D	A	I	S	L	S	V	G	D	H	F	G	K	G	853
AGA	GAA	TTA	AAT	TGT	GGA	GAT	GCC	ATA	TCT	CTT	TCT	GTG	GGA	GAT	CAC	TTT	GGA	AAA	GGG	2586
N	G	L	T	W	A	E	K	F	Q	C	E	G	S	E	T	H	L	A	L	873
AAT	GGT	CTA	ACT	TGG	GCC	GAA	AAG	TTC	CAG	TGT	GAA	GGG	AGT	GAA	ACT	CAC	CTT	GCA	TTA	2646

Fig. 2E



C	P	I	V	Q	H	P	E	D	T	C	I	H	S	R	E	V	G	V	V	893
TGC	CCC	ATT	GTT	CAA	CAT	CCG	GAA	GAC	ACT	TGT	ATC	CAC	AGC	AGA	GAA	GTT	GGA	GTT	GTC	2706
C	S	R	Y	T	D	V	R	L	V	N	G	K	S	Q	C	D	G	Q	V	913
TGT	TCC	CGA	TAT	ACA	GAT	GTC	CGA	CTT	GTG	AAT	GGC	AAA	TCC	CAG	TGT	GAC	GGG	CAA	GTG	2766
E	I	N	V	L	G	H	W	G	S	L	C	D	T	H	W	D	P	E	D	933
GAG	ATC	AAC	GTG	CTT	GGA	CAC	TGG	GGC	TCA	CTG	TGT	GAC	ACC	CAC	TGG	GAC	CCA	GAA	GAT	2826
A	R	V	L	C	R	Q	L	S	C	G	T	A	L	S	T	T	G	G	K	953
GCC	CGT	GTT	CTA	TGC	AGA	CAG	CTC	AGC	CTG	GGG	ACT	GCT	CTC	TCA	ACC	ACA	GGA	GGA	AAA	2886
Y	I	G	E	R	S	V	R	V	W	G	H	R	F	H	C	L	G	N	E	973
TAT	ATT	GGA	GAA	AGA	AGT	GTT	CGT	GTG	TGG	GGA	CAC	AGG	TTT	CAT	TGC	TTA	GGG	AAT	GAG	2946
S	L	L	D	N	C	Q	M	T	V	L	G	A	B	P	C	I	H	G	N	993
TCA	CTT	CTG	GAT	AAC	TGT	CAA	ATG	ACA	GTT	CTT	GGA	GCA	CCT	CCC	TGT	ATC	CAT	GGA	AAT	3006
T	V	S	V	I	C	T	G	S	L	T	Q	P	L	F	P	C	L	A	N	1013
ACT	GTC	TCT	GTG	ATC	TGC	ACA	GGA	AGC	CTG	ACC	CAG	CCA	CTG	TTT	CCA	TGC	CTC	GCA	AAT	3066
V	S	D	P	Y	L	S	A	V	P	E	G	S	A	L	I	C	L	E	D	1033
GTA	TCT	GAC	CCA	TAT	TTG	TCT	GCA	GTT	CCA	GAG	GGC	AGT	GCT	TTG	ATC	TGC	TTA	GAG	GAC	3126
K	R	L	R	L	V	D	G	D	S	R	C	A	G	R	V	E	I	Y	H	1053
AAA	CGG	CTC	CGC	CTA	GTG	GAT	GGG	GAC	AGC	CGC	TGT	GCC	GGG	AGA	GTA	GAG	ATC	TAT	CAC	3186

Fig. 2F



D G F W G T I C D D G W D L S D A H V V 1073
 GAC GGC TTC TGG GGC ACC ATC TGT GAT GAC GGC TGG GAC CTG AGC GAT GCC CAC GTG GTG 3246

 C Q K L G C G V A F N A T V S A H F G E 1093
 TGT CAA AAG CTG GGC TGT GGA GTG GCC TTC AAT GCC ACG GTC TCT GCT CAC TTT GGG GAG 3306

 G S G P I W L D D L N C T G T E S H L W 1113
 GGG TCA GGG CCC ATC TGG CTG GAT GAC CTG AAC TGC ACA GGA ACG GAG TCC CAC TTG TGG 3366

 Q C P S R G W G Q H D C R H K E D A G V 1133
 CAG TGC CCT TCC CGC GGC TGG GGG CAG CAC GAC TGC AGG CAC AAG GAG GAC GCA GGG GTC 3426

 I C S E F T A L R L Y S E T E T E S C A 1153
 ATC TGC TCA GAA TTC ACA GCC TTG AGG CTC TAC AGT GAA ACT GAA ACA GAG AGC TGT GCT 3486 18 / 95

 G R L E V F Y N G T W G S V G R R N I T 1173
 GGG AGA TTG GAA GTC TTC TAT AAC GGG ACC TGG GGC AGC GTC GGC AGG AGG AAC ATC ACC 3546

 T A I A G I V C R Q L G C G E N G V V S 1193
 ACA GCC ATA GCA GGC ATT GTG TGC AGG CAG CTG GGC TGT GGG GAG AAT GGA GTT GTC AGC 3606

 L A P L S K T G S G F M W V D D I Q C P 1213
 CTC GCC CCT TTA TCT AAG ACA GGC TCT GGT TTC ATG TGG GTG GAT GAC ATT CAG TGT CCT 3666

 K T H I S I W Q C L S A P W E R R I S S 1233
 AAA ACG CAT ATC TCC ATA TGG CAG TGC TCT GCC CCA TGG GAG CGA AGA ATC TCC AGC 3726

Fig. 2G



P	A	E	E	T	W	I	T	C	E	D	R	I	R	V	R	G	G	D	T	1253
CCA	GCA	GAA	GAG	ACC	TGG	ATC	ACA	TGT	GAA	GAT	AGA	ATA	AGA	GTG	CGT	GGA	GGA	GAC	ACC	3786
E	C	S	G	R	V	E	I	W	H	A	G	S	W	G	T	V	C	D	D	1273
GAG	TGC	TCT	GGG	AGA	GTG	GAG	ATC	TGG	CAC	GCA	GGC	TCC	TGG	GGC	ACA	GTG	TGT	GAT	GAC	3846
S	W	D	L	A	E	A	E	V	V	C	Q	Q	L	G	C	G	S	A	L	1293
TCC	TGG	GAC	CTG	GCC	GAG	GCG	GAA	GTC	GTG	TGT	CAG	CAG	CTG	GGC	TGT	GGC	TCT	GCT	CTG	3906
A	A	L	R	D	A	S	F	G	Q	G	T	G	T	I	W	L	D	D	M	1313
GCT	GCC	CTG	AGG	GAC	GCT	TCG	TTT	GGC	CAG	GGA	ACT	GGA	ACC	ATC	TGG	TTG	GAT	GAC	ATG	3966
R	C	K	G	N	E	S	F	L	W	D	C	H	A	K	P	W	G	Q	S	1333
CGG	TGC	AAA	GGA	AAT	GAG	TCA	TTT	CTA	TGG	GAC	TGT	CAC	GCC	AAA	CCC	TGG	GGA	CAG	AGT	4026
D	C	G	H	K	E	D	A	G	V	R	C	S	G	Q	S	L	K	S	L	1353
GAC	TGT	GGA	CAC	AAG	GAA	GAT	GCT	GGC	GTG	AGG	TGC	TCT	GGA	CAG	TCG	CTG	AAA	TCA	CTG	4086
N	A	S	S	G	H	L	A	L	I	S	S	I	F	G	L	L	L	L	1373	
AAT	GCC	TCC	TCA	GGT	CAT	TTA	GCA	CTT	ATT	TTA	TCC	AGT	ATC	TTT	GGG	CTC	CTT	CTC	CTG	4146
V	L	F	I	L	F	L	T	W	C	R	V	Q	K	Q	K	H	L	P	L	1393
GTT	CTG	TTT	ATT	CTA	TTT	CTC	ACG	TGG	TGC	CGA	GTT	CAG	AAA	CAA	AAA	CAT	CTG	CCC	CTC	4206
R	V	S	T	R	R	R	G	S	L	E	E	N	L	F	H	E	M	E	T	1413
AGA	GTT	TCA	ACC	AGA	AGG	AGG	GGT	TCT	CTC	GAG	GAG	AAI	TTA	TTC	CAT	GAG	ATG	GAG	ACC	4266

Fig. 2H



C L K R E D P H G T R T S D D T P N H G 1433
TGC CTC AAG AGA GAG GAC CCA CAT GGG ACA AGA ACC TCA GAT GAC ACC CCC AAC CAT GGT 4326

C E D A S D T S L L G V L P A S E A T K 1453
TGT GAA GAT GCT AGC GAC ACA TCG CTG TTG GGA GTT CTT CCT GCC TCT GAA GCC ACA AAA 4386

*

TGA

1454
4389

CTTAGACTCCAGGGCTCACCGATCAACCTCTAAATACTTTGAAGGAGACAACCTTAATGAATAAGAGGA 4468
AGTCAAGTTGCCCTATGGAAAACCTTGTCCTAACATTCTTGAACATAAGCTAACAGGAAACAGCTAAATTGATAAAAGACTGG 4547
TGATAATAAAAATTGAATTATGTATCTACTGTTAAAAAAACGGACCCGTTGGGTGCG 4626
AC

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4628

Fig. 2I

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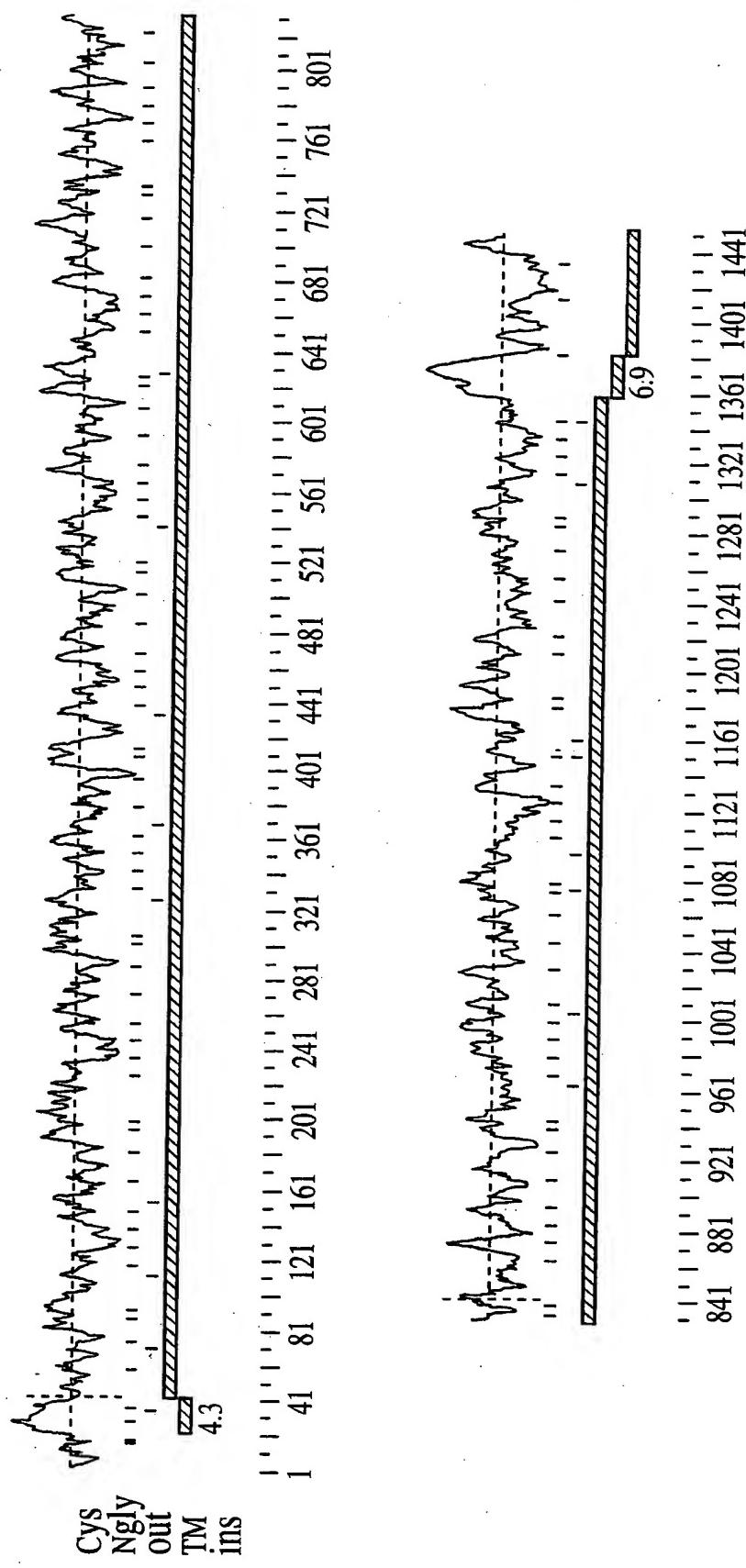


Fig. 2J



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10	20	30	40	50	60	70
Hum.	MMLPQNSWHIDEGRCCCHQNLFSAVVTCILLNSCFLISSFNGTDLLELRVLNVNGDPCSGTVEVKFQQGQWG					
:	::	::	::	::	::	::
WC1	MAL-----GR---HLSLRGL---CVLLGT--MVG---GQAELRLKDGVHRCEGRVEVKHQGEWG	10	20	30	40	50
80	90	100	110	120	130	
Hum.	TVCDDGWNTTASTVVCKQLGCCPFSSFAMERFGQAVTR-HGKIWLDDVSCYGNESALMWCQH---REWGSHN					
:	::	::	::	::	::	::
WC1	TVDGYRWTILKDAVVCRQLGCAGAIG-FPGGAYFGPGLGPPIWLLYTSCSEGTESTVSDEHSNIKDYRNDG	60	70	80	90	100
140	150	160	170	180	190	200
Hum.	CYHGEDVGVNCYGEANLGLRLVDGNNSSGRVEVKFQERWGTICDDGWNLNNTAAVVCRLQLGCPSSFISSG					
:	::	::	::	::	::	::
WC1	YNHGRDAGVVCSG-----FVRLAGGDGPCSGRVEVHSGEAWIIPVSDGNFTLATAQIIICAELGGKAVSVLG	120	130	140	150	160
210	220	230	240	250	260	270
Hum.	VVNNSPAVLRPPIWLDDILCQGNELIALWNCRHRGWNHDCSHNEDVTLTCYDSSDLELRVLVGGTNRCMGRVE					
:	::	::	::	::	::	::
WC1	HELFRESSAQVWAEEFRCEGEPELWVCPRVPCPGGTCHHSGSAQVVCSAYSEVRL-MTNGSSQCEGQVE	190	200	210	220	230

Fig. 2K



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280	290	300	310	320	330	340		
Hum.	LKIQGRWGTVCHKWNNAAADVVCKQLGCGTALHFAGLPHLQSGLPHVSCSGNESFLWDCRHSgt							
WC1	MNISGQWRALCASHWSLANANVICRQLGGCGVAISTPQQPHLVEEGDQILTARFHCSGAESFLWSCPVTAL							
	260	270	280	290	300	310	320	
350	360	370	380	390	400	410		
Hum.	VNFIDCLHQNDVSVICSDGADLELRADGSNNCSGRVEVRTHEQWWTTICDQNWKNEQALVVCKQLGCPFSV							
WC1	GGPDCCSHGNNTASVICS-GNQI-----							
	330	340					350	
420	430	440	450	460	470	480		
Hum.	FGSRRAKPSNEARDIWINSISCTGNESALWDCTYDGKAKRTCFRRSDAGVICSDFADLDLRLVGAHSPCY							
WC1	-----SQPTGSA-----ASEDSA-----PY-----							
	360						370	380
490	500	510	520	530	540	550		
Hum.	GRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSIGNESNIWDCE							
WC1	GRVEILDQGSWGTICDDGWDDARVVCRQLGCGEALNATGSAHFGAGSGPIWLDNINCTGKESHVWRCP							
	390	400	410	420	430	440	450	

Fig. 2L



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560	570	580	590	600	610	620
Hum.	HSGWGXHNCVHREDVIVTCSSGDATAWGLRLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKAAAVVCSQLDC					
WC1	SRGWGQHNCRHKQDAGVICs--EFLALRMVSEDQQCAGWLEVFYNGTWGSVCRNPMEDITVSTICRQLGC					
460	470	480	490	500	510	520
630	640	650	660	670	680	690
Hum.	PSSIIGMGLGNASTGYGKIWLDDVSCDGDESSDLWSCRNSGWGNNDCSHSEDGVVICSDASDMELRLVGGS					
WC1	GDSGTLNSSVALREGFRPQWVDRIQCRKTDITSIWLQCPSPDPWNYNNSCSPKEEAYIWCADSR--QIRLVDDGG					
530	540	550	560	570	580	590
700	710	720	730	740	750	760
Hum.	SRCAGKVEVNQGAVGILCANGWMNIAEVVCRQLECGSAIRVSREPHFFTERTLHILMSNSGCTGGAEASL					
WC1	GRCSSGRVEILDQGSWGTICCDRDLDDARVVCKQLGCGEALDAVSSFFGTGSGPPIWLDEVNCRGEESQV					
600	610	620	630	640	650	660
770	780	790	800	810	820	830
Hum.	WDCIRREWKTACHLNMEASLICSAHRQPRILVGADMPCSGRVEVKHADTWRSVCDSDFLHAAANVLCREL					
WC1	WRCPSSWGWRQHNCNHFQEDAGVICSGF--VRIAGGDGPCSGRVEVHSGEAWTPVSDGNFTLPTAQVICAEEL					
670	680	690	700	710	720	730

Fig. 2M



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Fig. 2N



1120 1130 1140 1150 1160 1170 1180
Hum. PSRGWQHDCRHKE DAGVICSEFTAIRLYSETETESCAGRLEVFYNGTWGSVGRNNTTIAAGIVCROLG
::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
WC1 PSRGWGRHDCRHKE DAGVICSEFLALRMVSEDQQ--CAGWLEVFYNGTWGSVCRSPMEDITVSVICRQLG
1020 1030 1040 1050 1060 1070

1190 1200 1210 1220 1230 1240
Hum. CGENGVVSLAPLSKRTGSGFMWVDDIQCPKTHISIWIQCLSAPWERRISSPAEETWITCEDR-----
::: ::: ::
WC1 CGDSSILNTSVGLREGSRPRWVDLIIQCRKMDTSWLQCPSPGWPKYSSSCSPKEEAYISCEGRRPKSCTAAA
1080 1090 1100 1110 1120 1130 1140

1250 1260 1270 1280 1290 1300
Hum. -----IRVRGGDTECSGRVEIWHAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIW
::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
WC1 CTDREKLRLGGDSECSGRVEVWHNGSWGTVCDDSSWLSLAEAEVVCQQLGCGQALEAVRSAAFGPNGNSIW
1150 1160 1170 1180 1190 1200 1210

1310 1320 1330 1340 1350 1360
Hum. LDDMRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCSG-----QSLKSLNASSGHLALI
::: ::
WC1 LDEVQCGGRESSLWDCVAEPWGQSDCKHEEDAGVRCSGVRTTLPTTTAGTRTSNSLEPGIFSLPGVLCLI
1220 1230 1240 1250 1260 1270 1280

Fig. 20



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Hum.	LSSIFGLLVLVLFILFLTWCRVQK	1370	1380	1390	1400	1410
:.....:.....:.....:		:.....:.....:.....::.....:.....:.....:	
WC1	LGSLLFLVLVILVTQLLRW-RAERRALSSYEDALAEAVYEEFDYLLTQKEGLGSPDQMTDVPDENYYDDAE	1290	1300	1310	1320	1330
Hum.	TC-----LKREDPHGTRTSD-----	1420	1430	1440	1450	
:.....:.....:.....:		:.....:.....:.....::.....:.....:.....:	
WC1	EVPVPGTPSPSQQGNNEEVVPPEKEDGVRSQSQTGSFLNFSREAANPGEGEESFWLLQGKKGDAGYDDVELSA	1360	1370	1380	1390	1400
Hum.	LPASEAT-K					
:.....:.....:.....:		:.....:.....:.....::.....:.....:.....:	
WC1	LGTSSPVTFES					

Fig. 2P



Hum. ATGATGCTGCCCTCAAAACTCGTGGCATATTGATTGGAAGATGCTGTCATCAGAACCTTTCTCTG ::::: ::::: WC1 ATG-----GCTC-TGG-----GCAGACA-----CCTCT-CCCTG	10 80 90 100 110 120 130 140 Hum. CTGTGGTAACCTTGCATCCTGCCATTCTGCTCATTCTCATCAGCAGTTAATGGAACAGATTGGA ::::: WC1 C-GGGGACTCT-GTGTCCCTCCTCCT-----CGGCA-----CATGGTGGTGGTCAAGCTCTGGA	10 40 50 60 70 80 150 160 170 180 190 200 210 Hum. GTTGAGGCTGGTCAATGGAGACGGTCCCCCTGGACAGTGGAGGTGAATACTCCAGGGACAGTGGGG ::::: WC1 GCTGAGGTGAGGATGGCATCGCTGTGAGGGAGAGTGGAAAGTGAAGCACCCAAGGAGAATGGGC	90 100 110 120 130 140 150 220 230 240 250 260 270 Hum. ACTGGTGTGATGGTGGAAACACTACTGCCCT-CAACTGTCGTGGCAAACAGCTGGATGTCCATT ::::: WC1 ACAGTGGATGGTTACAGGTGGA-CATTGAAGGATGCACTGTAGTGTGGAGCTGGAGCTGGAGCT	160 170 180 190 200 210
--	---	---	---	-------------------------

Fig. 2Qi



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280	290	300	310	320	330	340
Hum.	TCTTTCGCCCATGTTCGACAAAGCCGTGA--	CTAGACATGGAAAAATTGGCTTGATGATGTTTC				
WC1	GCCATTG--GT	TTCTGGAGGGCTTATTGGCCAGGACTTGGCCCCATTGGCTTTGTATACTTC				
220	230	240	250	260	270	280
350	360	370	380	390	400	410
Hum.	CTGTTATGGAAATGAGTCAGCTCTGGAAATGTCAACACCAGGAATGGGAAGGCCATAACTGTTATCAT					
WC1	ATGTAAGGGACAGAGTCAACTGTCAGTGACTGTGAGCATTCTAATATTAAAGAC-TATC-GTAATGAT					
290	300	310	320	330	340	350
420	430	440	450	460	470	480
Hum.	GGAGAACATGTTGGTGAACCTGTTATGGTGAAGCCAA-TCTGGGTTTGAG--GCTAG-TGGATGGAAAC					
WC1	GGCTATAATCATGGTCGGA---TGCTGGAGTAGTCTGCTCAGGATTGTGCCTGGCTGGAGGGATG					
360	370	380	390	400	410	420
490	500	510	520	530	540	550
Hum.	AACTCCTGTTCAAGGAGAGTGGAGGTGAATAAGGTTGGGGACTATATGTGATGGGTGGA					
WC1	GAC-CCTGCTCAGGGCGAGTAGAAGTCATT--CTGGAGAACGCTTGGATCCCAGTGT-CTGATGGAACT					
430	440	450	460	470	480	

Fig. 2Qii



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Hum.	ACTTGAATACTGCCGTGGTGTGCAGGCAACTAGGATGTCCATCTTCTGGAGTTGT ::: : : WC1 TCACACTGCCACTGCC-----CAG-----ATCATCTGT	560 570 580 590 600 610 620 490 500 510 520
Hum.	TAATAGCCCTGCTATTGCCGCCATTGGCTGGATGACATTTATGCCAGGGAAATGAGTTGGCACT- ::: : WC1 TTGTTGGC-----AAGGCTG---TGTCTGT-----CCTGGGACATGAG---CTCTT	630 640 650 660 670 680 690 530 540 550 560
Hum.	CTGGAAATTGCAGACATCGTGGATGGGAAATCATGACTGCAGTCACAATGAGGATGTCACTTAACTTGT ::: : : WC1 CAGAGAGTCCAGT-GCC-----CAGGTCTG---GGC---TGAAGAGTTCA-----GG	700 710 720 730 740 750 760 570 580 590 600
Hum.	TATGATAGTAGTGATCTTGAACTAAGGCTTGAGGTGAAACTAACCGCTGTATGGGAGAGTAGAGCTGA ::: : : : WC1 TGTGAGGGGGAGGAGCCTGAGCT---CT-----GGGTCTGCC-CAGATG-----CCCTG-	770 780 790 800 810 820 830 610 620 630 640 650

Fig. 2Qiii



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Hum. AAATCCAAGGAAGGGTGGGGACCGTATGCCACCATAAAGTGGAAACAATGCTGCAGCTGATGCTATGCCAA ::::: WC1 ----TCCA-----GGGGCACGTGT--CACCACA-GTGGATC--TGCT-CAGGTTGTTGTTAGGCAT 660 670 680 690 700	840 850 860 870 880 890 900 910 920 930 940 950 960 970	Hum. GCAGTTGGATGTGGAACCGCACTTCACCTCGCTGGCTCATTGCAGTCAGGGTCTGATGTTGTA ::: WC1 ACT----CAGAAGTCCGGCTCATGACAA-AC-GGCT--CCTC-TTAG-TGTGAAGGGCAGGTGGAGAT 710 720 730 740 750 760	980 990 1000 1010 1020 1030 1040 Hum. TGGCTTGTGGTCTCCCTGCTCCGTAATGAAATCTTTCTTGGACTGCAGACATTCCGAAACCGTCA ::: WC1 GAACATT-----TCTG-GACAATGGAGAGGGCTCTGTGCCTCCCC-ACTGGAGTCTGCCAATGCC---A 770 780 790 800 810 820	1050 1060 1070 1080 1090 1100 1110 Hum. ATTTGACTGTCTCATCAAAACGATGTGTCTGTGATCTGCTCAGATGGAGCAGATTGGAAC TGCGACT ::: WC1 ATGTTATCTGTCGTAGCTCGGCTGTGGAGTTGCCATCTCCACCCCCGGAG-----GACCAC-ACT 830 840 850 860 870 880
--	--	--	---	--

Fig. 2Qiv



Fig. 2Qv



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Hum.	CTGGAGTAATTGTTCTGATAAGGCAGATCTGGACCTAAGGCTTGTCCCCCTCATAGCCCTGTTATGG	1400	1410	1420	1430	1440	1450	1460
WC1	CTCAGA-----CAG--CAGGCAGCTCCG--CCTGGTG---GACGGG-GC--GGTCCCIGGCCGG	1110		1120	1130	1140	1150	1160
Hum.	GAGATTGGAGGTGAATAACCAAGGAGAGTGGGGACTGTGTCACTGACAGATGGAGCACAAAGG-AATGC	1470	1480	1490	1500	1510	1520	
WC1	GAGAGTGGAGATCCTTGACCAGGGCTCCTGGGCACCATCTGTGATGACGGCTGGGAC-CTGGACGATGC	1170	1180	1190	1200	1210	1220	
Hum.	A-GCTGTTGTGTAACAATTGGGATGTGGA-AAGCCCTATGCATGTGTTGGTATGACCTATTAAAG	1530	1540	1550	1560	1570	1580	1590
WC1	CCGC-GTGGTGTGCAGGCAGCTGGCTGGAGAACGGCTCA-ATGCCACACGGGTCTGCTCACCTCGGGG	1230	1240	1250	1260	1270	1280	1290
Hum.	AAGGATCAGGACCTATTGGCTGGATGACGTTCTTGCATTGAAATGAGTCAAATACTGGGACTGTGA	1600	1610	1620	1630	1640	1650	1660
WC1	CAGGATCAGGGCCCATCTGGTGGACAACTTGAACCTGGCTGGAGTCCCCACGTTGGAGGTGCC	1300	1310	1320	1330	1340	1350	1360

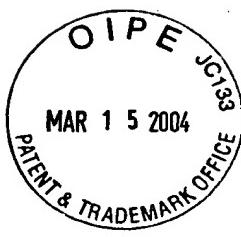
Fig. 2Qvi



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1670	1680	1690	1700	1710	1720	1730
Hum.	ACACAGTGGATGGGAAAGCATAATTGTGTACACAGAGGGATGTGATTGTAACCTGCTCAGGTGATGCA					
.
WC1	TTCCCCGGGCTGGGGCAGCACACTGCAGACACAAGCAGGACGGACGGGGTCATCTGCTCAG--AGTTC-					
1370	1380	1390	1400	1410	1420	1430
1740	1750	1760	1770	1780	1790	1800
Hum.	ACATGGGGCCTGAGGCTGGTGGCGGGCAGCAAACCGCTGCTCGGGAAGAACTGGAGGTGACTTTCAAGGAC					
.
WC1	-CT--GCCCTCAGGATGGTGAGTGAGGACCAGCAGTGTGGCTGGCTGGAAGTTTCTACAATGGGA					
1440	1450	1460	1470	1480	1490	1500
1810	1820	1830	1840	1850	1860	1870
Hum.	GGTGGGCACAGTGTGATGACGGCTGGAACAGTAAAGCTGCAGCTGTGGTGTAGCCAGCTGGACTG					
.
WC1	CCTGGGCAGTGTCTGCCGTAAACCCATGGAAGACATCACTGTCACGATCTGCAGACAGCTGGCTG					
1510	1520	1530	1540	1550	1560	1570
1880	1890	1900	1910	1920	1930	1940
Hum.	CCCATCTTCTATCATGGCATGGGTCTG-GGAAAACGCCCTCTA-CAGGATATGGAAAAATTGGCTCGATG					
.
WC1	T--GGGGACAGTGGAACCCCTCAACTCTCTGTTGCTCTTAGAGAAGGTTAGGCCACAGTGGGTGGAT-					
1580	1590	1600	1610	1620	1630	

Fig. 2Qvii



1950	1960	1970	1980	1990	2000	2010
Hum.	ATGTTCCCTGTGATGGAGATGAGTCAGATCTGGTCATGCAGGAACAGTGGTG--GGAAATAATGAC					
WC1	-AGAATCCAGTGTGGAAAAGTACACCTCT---CTGGCAGTGTGCCCTCTGACCCATTACAAC	1640	1650	1660	1670	1680
2020	2030	2040	2050	2060	2070	2080
Hum.	TGGAGTCACAGTGAAGATGTTGGAGTG-ATCTGTTCTGATG-CATCGGATATGGAGCTGAGGCTTGTGGG					
WC1	T-CATGCTCTCCAAAGGAGGAAGCCTATATCTGGTGTGCAGACAGCAGACA--GATCCGC--CTGGTGGGA	1710	1720	1730	1740	1750
2090	2100	2110	2120	2130	2140	2150
Hum.	TGGAAGCAGCAGGTGTGGAAAAGTTGAGGTGAATGTCAGGGTGGGAATTCTGTGCTTAAT					
WC1	TGGAGGTGGTCGCTCTGGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGCACCATCTGTGATGAC	1770	1780	1790	1800	1810
2160	2170	2180	2190	2200	2210	2220
Hum.	GGCTGGGAATGAACATGCTGAAGTTGTCAGGCCAACTTGAATGTTGGTCTGCAATCAGGGTCTCCA					
WC1	CGCTGGACCTGGACGATGCCCGTGGTGTGCAAGCAGCTGGGCTGTGGAGAACG---CCTGGACGCCA	1840	1850	1860	1880	1890

Fig. 2Qviii



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Hum.	GAGA-GCCTCATTTCACAGAA--AGAACATTACACATCTTAATGTCGAATTCTGGCTGGCAACTGGAGGGAA	2230	2240	2250	2260	2270	2280	
WC1	CTGTCCTCTTCCCTCTCGGGACGGGATCAGGGCCCCATCTGGCTGGATGAAGTCAACTGCAGAGGAGGAA	1910	1920	1930	1940	1950	1960	1970
Hum.	AGCCTCTCTGGATTACGATGGAGTTGGAAACAG-ACTGCGTGTCAATTAAATATGGAAGCAAG	2290	2300	2310	2320	2330	2340	2350
WC1	GTCCAAGATGGAGGTGCCCTCCCTGGGATGGCGGCAACACAAAC-TGCAAATCATCAAGAACATGCAGG	1980	1990	2000	2010	2020	2030	2040
Hum.	TTTGATCTGCTCAGCCCCACAGGCAGGCCAGGGCTGGTTGGAGCTGATATGCCCTGCTCTGGACGTGTTGAA	2360	2370	2380	2390	2400	2410	2420
WC1	AGTCATCTGCTCAGGATTGTGC-----GTCTGGCTGGAGGAGATGGACCCCTGCTCAGGGCGAGTAGAA	2050	2060	2070	2080	2090	2100	
Hum.	GTGAAACATGCAGACACATGGCGCTCTGTGATTCTGATTTCTCTCATGCTGCCAATGT--GCT	2430	2440	2450	2460	2470	2480	2490
WC1	GTGCATTCTGGAGAAGGCCTGGACCCCAAGTGTCTGATGGAAACCTCACACTCCCCACTGCCAGGTCACT	2110	2120	2130	2140	2150	2160	2170

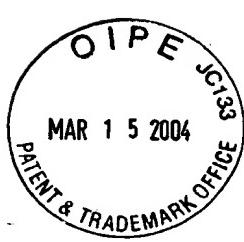
Fig. 2Qix



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Hum.	GTGCAGAGAATTAAATTGTGGAGATGCCATATCTCTTCTGTGGAGATCACTTTGAAAAAGGG-AATGG	2500	2510	2520	2530	2540	2550	2560
WC1	GTGCAGAGC--TGGATGTGGCAAGGCTGTCT-GTCCTGGACACATGCCATTCAAGAGTCCGATGG	2180	2190	2200	2210	2220	2230	2240
Hum.	TCTAACTTGGCCGAAAAGTCCAGTGTGAAGGGAGTGAAACTCACCTTGCAATTATGCCCATTTGTC	2570	2580	2590	2600	2610	2620	2630
WC1	CCAGGTCTGGCTGAAGAGTTCAGGTGTGAGGGGGAGCCTGAGCTCTGGCCTGCCAGAGTCCCC	2250	2260	2270	2280	2290	2300	2310
Hum.	CATCCGGAAGACACTTGTATCCACAGCAGAGAAAGTTGGAGTTGTCTGTTCCCGATATAAGATGTC	2640	2650	2660	2670	2680	2690	2700
WC1	TGTCCAGGAGGCACATGTCTCCACAGTGGAGCTGCTCAGGTGTGTTCAAGTGTACACAGAAGTCCAGC	2320	2330	2340	2350	2360	2370	2380
Hum.	TTGTGAATGGCAAATCC---CAGTGTGACGGCAAGTGGAGATCAACGTGCT-TGGACACTGGGGCTCAC	2710	2720	2730	2740	2750	2760	2770
WC1	TTATGAAAAACGGCACCTCTCAATGTGAGGGCAGGTGGAGAT-GAAGATCTTGACGATGGAGAGCC	2390	2400	2410	2420	2430	2440	2450

Fig. 2Qx



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Hum.	TGTGTGACACCCACTGGACCCAGAAGATGCCCGTGTCTATGCAGACAGCTCAGCTGGGACTGCTCT	2780	2790	2800	2810	2820	2830	2840
	::::: ::::: ::::: :::							
WC1	TCTGTGCCTCCCAC TGGAGTCTGGCCAATGCCAATGTTGTCTGTCGT CAGCTGGCTGGAGTCGCCAT	2460	2470	2480	2490	2500	2510	2520
Hum.	CTCAACCACAGGAGAAAATATTGGAGAAAGAAGTGTCCGTGTGGGACACAGGTTCAT TGCTTA	2850	2860	2870	2880	2890	2900	2910
	::::: ::::: ::::: :::							
WC1	CTCCACCCCCAGAGGACACACTTGGTGGAAAGGAGGTGATCAGATCTCAACAGCCCATTCACTGCTCA	2530	2540	2550	2560	2570	2580	2590
Hum.	GGGAATGAGTCACTTCTGGATAACTGTCAAATGACAGTTCTTGAGCACCTCCCTGTATCCATGGAAATA	2920	2930	2940	2950	2960	2970	2980
	::::: ::::: ::::: :::							
WC1	GGGGCTGAGTCCTTCCTGTGGAGTTGCCTGTGACTGCCTGGGTGGCCTGACTGTCCCCATGGCAACA	2600	2610	2620	2630	2640	2650	2660
Hum.	CTGTCTGTGATCTGCACAGGAAGGCCACTGACCCAGCTGACCTGGCTGGCAAATGTATCTGACCC	2990	3000	3010	3020	3030	3040	3050
	::::: ::::: ::::: :::							
WC1	CAGCCTCTGTGATCTGCTCAGGAAACCCAGGTGCTGCCCAAGTGCACCGACTTCCCTGTCTCAACC	2670	2680	2690	2700	2710	2720	2730

Fig. 2Qxi



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Hum.	ATATTGCTGCAGTCCAGAGGGCAGTGCTTGATCTGCTTAGGGACAAACGGCTCCGCCTAGTGGAT	3060	3070	3080	3090	3100	3110	3120
.	· · : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · :
WC1	TGCAGGCTCTGGGCCCTCAGAGGAGGTCCCTACTGCTCAGACAGCAGGCAAGGCTCCGCCTGGTGGAC	2740	2750	2760	2770	2780	2790	2800
Hum.	GGGACAGCCGGCTGTGCCGGAGAGTAGAGATCTATCACGACGGCTTCTGGGGCACCATCTGTGATGACG	3130	3140	3150	3160	3170	3180	3190
.	· : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · :
WC1	GGGGGGGTCCCTGCGGGAGAGTTGAGATCCTTGACCAGGGCTCCTGGGCACCATCTGTGATGATG	2810	2820	2830	2840	2850	2860	2870
Hum.	GCTGGGACCTTGAGCGATGCCAACGTTGTCAAAAGCTGGCTGTGGAGTGGCTCAATGCCACGGT	3200	3210	3220	3230	3240	3250	3260
.	· : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · :
WC1	ACTGGGACCTGGACGATGCCCGTGTGGCTGCAGGCAGCTGGCTGTGGAGAAGGCCCAATGCCACGGG	2880	2890	2900	2910	2920	2930	2940
Hum.	CTCTGCTCACTTGGGAGGGTCAGGGCCATCTGGCTGGATGACCTGAACCTGCACAGGAACGGAGTCC	3270	3280	3290	3300	3310	3320	3330
.	· : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · : · :
WC1	GTCTGCTCACTTGGGGCAGGATCAGGGCCATCTGGCTGGACGACCTGAACCTGCACAGGAAGGAGTCC	2950	2960	2970	2980	2990	3000	3010

Fig. 2Qxii



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Hum.	CACTTGTGGCAGTGCCTTCCC GGCTTGGGGCAGGCACGCACTGCAGGCACAAGGAGGACGGCAGGGTCA	3340	3350	3360	3370	3380	3390	3400
WC1	CACGTGTGAGGTGCCCTCCGGGCTTGGGGCAGGCACGCACTGCAGACACAAGGAGGACGCCGGGTCA	3020	3030	3040	3050	3060	3070	3080
Hum.	TCTGCTCAGAATTCACAGCCTTGAGGCTTACAGTGAACAGAGACTGAAACAGAGGCTGTGGAGATTGGA	3410	3420	3430	3440	3450	3460	3470
WC1	TCTGCTCAGAGTTCCCTGGCCCTCAGGAT---GGTAG-CGAGGACCCAGCAG-TGTGCTGGGTGGCTGGA	3090	3100	3110	3120	3130	3140	
Hum.	AGTCTTCTATAACGGGACCTGGGCAGCGTCGGCAGGAAACATCACCACAGCCATAGCAGGCATTGTG	3480	3490	3500	3510	3520	3530	3540
WC1	GGTTTCTACAACGGGACCTGGGCAGTGTCTGGCAGCCCCATGGAAGATACTGTCCTGGCTGATC	3150	3160	3170	3180	3190	3200	3210
Hum.	TGCAGGGCAGCTGGGCTGTGGGAGAATGGAGTTGTAGCCTCGCCCCCTTA--TCT-AAGACAGGGCTCTG	3550	3560	3570	3580	3590	3600	
WC1	TGCAGACAGCTGGATGTGGGACAGTGGA--AGTCT-CAACACCTCTGTGGTCTCAGGGAAAGGTTCTA	3220	3230	3240	3250	3260	3270	3280

Fig. 2Qxiii



3610	3620	3630	3640	3650	3660	3670
Hum.	GTTTCATGGGGTGGATGACATTCAAGTGTCTAAAACGCATATCTCCATATGGCAGTGCCTGTC					
WC1	GACCCGGTGGGTAGATTAAATTCAAGTGTGGAAAATGGATACCTCTCTGGCAGTGCCTGTC					
3290	3300	3310	3320	3330	3340	3350
3680	3690	3700	3710	3720	3730	3740
Hum.	ATGGGAGCGAAGAACATCTCCAGCCCCAGCAGAAGAGACCTGGGATCACATGTGAAGATAATA					
WC1	ATGAAATACAGTTCATGCTCTCCAAAGGAGGAAGCCTACATCTCATGTGAAGGAAGAACCAAGAGC					
3360	3370	3380	3390	3400	3410	3420
3750	3760					
Hum.	-----TGC-----					
WC1	TGTCCAACGTGCGCCTGCACAGGACAGAGAAGGCTCCGCCCTCAGGGAGACAGCGAGTGCTCAG					
3430	3440	3450	3460	3470	3480	3490
3770	3780	3790	3800	3810	3820	3830
Hum.	GGAGAGTGGAGATCTGGCACGGCAGGGCTCCTGGGACAGTGTGATGACTCTGGACCTGGCGAGGC					
WC1	GGCGGGTGGAGGTGGCACAAACGGCTCCCTGGGACCCGTGTGCATGACTCTGGAGGCCTGGCAGAGGC					
3500	3510	3520	3530	3540	3550	3560

Fig. 2Qxiv



3840	3850	3860	3870	3880	3890	3900
Hum.	GGAAAGTGGTGTTCAGCAGCTGGGCTGTGGCTCTGGCTCTGGCTCGAGGGACGCTTCGTTGCCAG					
WC1	TGAGGTGGTGTTCAGCAGCTGGGCTGTGGCCAGGCCCTGGAAAGCCGTGCAGCATTTGCCCT					
	3570	3580	3590	3600	3610	3620
						3630
3910	3920	3930	3940	3950	3960	3970
Hum.	GGAAACTGGAACCATCTGGTTGGATGACATGGGGTGCAGAAATGAGTCATTTCATTGGACTGTCAAG					
WC1	GGAAATGGAGGCATCTGGCTGGACGGAGGTGCAGTGCGGGGGGGAGTCCTCCCTGTGGACTGTGTTG					
	3640	3650	3660	3670	3680	3690
						3700
3980	3990	4000	4010	4020	4030	4040
Hum.	CCAAACCCCTGGGACAGAGTGACTGTGGACACAAGGAAGATGGCTGGGTGAGGTGCTGG---ACAGTC					
WC1	CGGAGCCCCCTGGGGCAGAGCGACTGCAAGCACGAGGGAGATGGCTGGTGAAGGTGCTGTAAAGGAC					
	3710	3720	3730	3740	3750	3760
						3770
4050	4060		4070		4080	4090
Hum.	G-----CTGAAATCACTGAATG--CCT-----CCTCAGGT-CATT---TAGCA-CTTATTATCCA					
WC1	AACATTGCCACGACCACAGCAGGGACCAACAACTCAAATTCTCCCTGGCATCTCCCTGCCT					
	3780	3790	3800	3810	3820	3830
						3840

Fig. 2QXV



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Hum.	G-----TATCTT-----GGGCTC-CTTCTC---CTGGTTCT-----GTTATTCTATTCTCA	4100	4110	4120	4130	4140
:	: : : : : : : : : : : :					
WC1	GGGGTTCTCTGCCTTATCCCTGGGGTGGCTCTCGGTCCGTATCCGTGACTCAGGCTACTCA	3850	3860	3870	3880	3890
						3900 3910
Hum.	CGTGGTG--CCGAGTTCAGAAAAACATCT-----GCCCT-----CT-----CAGAGTTT-----	4150	4160	4170	4180	
:	: : : : : : : : : : : :					
WC1	GATGGAGGAGGCAGAGCCTTATCCAGCTATGAAGATGCTCTGCTGAAGCTGTATGAGGAGCT	3920	3930	3940	3950	3960 3980
Hum.	-----CAAC-----CAGAAGGAGGG---GTTCT-CTCG-----AGGAGAATTATTCCATGA-----	4190	4200	4210	4220	
:	: : : : : : : : : : : :					
WC1	CGATTACCTTCTGACACAGAAAGGAAGGCTGGGCAGCCCAGATCAGATGACTGATGTCCTGATGAAAT	3990	4000	4010	4020	4030 4040
						4050
Hum.	----GATGGAG-----ACCTG-----CCTC-----AAGAGAGAGGAC	4230	4240	4250		
:	: : : : : :					
WC1	TATGATGATGCTGAAGAACGAGTACCAACTGGAAACTCCTTCAGGGAAATGAGGAGGAAGTGC	4060	4070	4080	4090	4100 4110 4120

Fig. 2Qxvi



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Fig. 2Qxvii



M	A	L	P	A	L	G	L	D	P	W	S	12	
GTCGACCCACCGCTCCGGCTGTGGCTGAGC	ATG	GCC	CTC	CCA	GCC	CTG	GGC	CTG	GAC	CCC	TGG	AGC	67
L	L	G	L	F	L	F	Q	L	L	P	T	T	32
CTC	CTG	GGC	CTT	TTC	CTC	TTC	CAA	CTG	CTG	CTG	CTG	CGG	127
G	G	G	Q	G	P	M	P	R	V	R	Y	A	52
GGA	GGC	GGG	CAG	GGG	CCC	ATG	CCC	AGG	GTC	AGA	TAC	TAT	187
L	S	F	F	H	Q	K	G	L	Q	D	F	D	72
CTT	AGC	TTC	TTC	CAC	CAG	AAG	GGC	CTC	CAG	GAT	TTT	GAC	247
G	N	T	L	Y	V	G	A	R	E	A	I	L	112
GGA	AAT	ACT	CTC	TAC	GTG	GGG	GCT	CGA	GAA	GCC	ATT	CTG	367
G	V	P	R	L	K	N	M	I	P	W	P	A	92
GGG	GTC	CCC	AGG	CTA	AAG	AAC	ATG	ATA	CCG	TGG	CCA	GCC	95
C	A	F	K	K	K	S	N	E	T	Q	C	F	132
TGT	GCC	TTT	AAG	AAG	AAG	AGC	AAT	GAG	ACA	CAG	TGT	TTC	427
S	Y	N	V	T	H	L	Y	T	C	G	T	F	152
TCT	TAC	AAT	GTC	ACC	CAT	CTC	TAC	ACC	TGC	GGC	ACC	TTC	487
F	I	E	L	Q	D	S	Y	L	L	P	I	S	172
TTC	ATT	GAA	CTT	CAA	GAT	TCC	TAC	CTG	TTG	CCC	ATC	TCG	547

Fig. 3A



K	G	Q	S	P	F	D	P	A	H	K	H	T	A	V	L	V	D	G	M	192	
AAA	GGC	CAA	AGC	CCC	TTT	GAC	CCC	GCT	CAC	AAG	CAT	ACG	GCT	GTC	TTG	GTG	GAT	GGG	ATG	607	
L	Y	S	G	T	M	N	N	F	L	G	S	E	P	I	L	M	R	T	L	212	
CTC	TAT	TCT	GGT	ACT	ATG	AAC	AAC	TTC	CTG	GGC	AGT	GAG	CCC	ATC	CTG	ATG	CGC	ACA	CTG	667	
G	S	Q	P	V	L	K	T	D	N	F	L	R	W	L	H	H	D	A	S	232	
GGA	TCC	CAG	CCT	GTC	CTC	AAG	ACC	GAC	AAC	TTC	CTC	CGC	TGG	CTG	CAT	CAT	GAC	GCC	TCC	727	
F	V	A	A	I	P	S	T	Q	V	V	Y	F	F	F	E	E	T	A	S	252	
TTT	GTG	GCA	GCC	ATC	CCT	TCG	ACC	CAG	GTC	GTC	TAC	TTC	TTC	GAG	GAG	ACA	GCC	AGC	787		
E	F	D	F	E	R	L	H	T	S	R	V	A	R	V	C	K	N	D	272		
GAG	TTT	GAC	TTC	TTT	GAG	AGG	CTC	CAC	ACA	TCG	CGG	GTG	GCT	AGA	GTC	TGC	AAG	AAT	GAC	847	
V	G	G	E	K	L	Q	K	W	T	T	F	L	K	A	Q	L	L	D	46 / 95		
GTG	GGC	GGA	AAG	CTG	CTG	CAG	AAG	AAG	TGG	ACC	ACC	TTC	CTG	AAG	GCC	CAG	CTG	CTC	907		
C	T	Q	P	G	Q	L	P	F	N	V	I	R	H	A	V	L	P	A	312		
TGC	ACC	CAG	CCG	GGG	CAG	CTG	CCC	TTC	AAC	GTC	ATC	CGC	CAC	GCG	GTC	CTG	CTC	CCC	GCC	967	
D	S	P	T	A	P	H	I	Y	A	V	F	T	S	Q	W	Q	V	G	G	332	
GAT	TCT	CCC	ACA	GCT	CCC	CAC	ATC	TAC	GCA	GTC	TTC	ACC	TCC	CAG	TGG	CAG	GTC	GGC	GGG	1027	
T	R	S	S	A	V	C	A	F	S	L	L	D	I	E	R	V	F	K	G	352	
ACC	AGG	AGC	TCT	GGG	GTT	TGT	TGT	GCC	TTC	TCT	CTC	TTG	GAC	ATT	GAA	CGT	GTC	TTT	AAG	GGG	1087

Fig. 3B



K	Y	K	E	L	N	K	E	T	S	R	W	T	T	Y	R	G	P	E	T	372	
AAA	TAC	AAA	GAG	TTG	AAC	AAA	GAA	ACT	TCA	CGC	TGG	ACT	ACT	TAT	AGG	GGC	CCT	GAG	ACC	1147	
N	P	R	P	G	S	C	S	V	G	P	S	S	D	K	A	L	T	F	M	392	
AAC	CCC	CGG	CCA	GGC	AGT	TGC	TCA	GTG	GGC	CCC	TCC	TCT	GAT	AAG	GCC	CTG	ACC	TTC	ATG	1207	
K	D	H	F	L	M	D	E	Q	V	V	G	T	P	L	L	V	K	S	G	412	
AAG	GAC	CAT	TTC	CTG	ATG	GAT	GAG	CAA	GTG	GTG	GGG	ACG	CCC	CTG	CTG	GTG	AAA	TCT	GGC	1267	
V	E	Y	T	R	L	A	V	E	T	A	Q	G	L	D	G	H	S	H	L	432	
GTG	GAG	TAT	ACA	CGG	CTT	GCA	GTG	GAG	ACA	GCC	CAG	GGC	CTT	GAT	GGG	CAC	AGC	CAT	CTT	1327	
V	M	Y	L	G	T	T	G	S	L	H	K	A	V	V	S	G	D	S	452		
GTC	ATG	TAC	CTG	GGA	ACC	ACC	ACA	GGG	TCG	CTC	CAC	AAG	GCT	GTG	GTA	AGT	GGG	GAC	AGC	1387	
S	A	H	L	V	E	E	I	Q	L	F	P	D	P	E	P	V	R	N	L	472	
AGT	GCT	CAT	CTG	GTG	GAA	GAG	ATT	CAG	CTG	TTC	CCT	GAC	CCT	GAA	CCT	GTT	CGC	AAC	CTG	1447	
Q	L	A	P	T	Q	G	A	V	F	V	G	F	S	G	G	V	W	R	V	492	
CAG	CTG	GCC	CCC	ACC	CAG	GGT	GCA	GTG	TTT	GTA	GGC	TTC	TCA	GGG	GGT	GTC	TGG	AGG	GTG	1507	
P	R	A	N	C	S	V	Y	E	S	C	V	D	C	V	L	A	R	D	P	512	
CCC	CGA	GCC	AAC	TGT	AGT	GTC	TAT	GAG	AGC	TGT	GTG	GAC	TGT	GTC	CTT	GCC	CGG	GAC	CCC	1567	
H	C	A	W	D	P	E	S	R	T	C	C	L	L	S	A	P	N	L	N	532	
CAC	TGT	GGC	TGG	GAC	CCT	GAG	TCC	CGA	ACC	TGT	TGT	GGC	TCT	CTG	CTG	CTG	CCC	AAC	CTG	AAC	1627

Fig. 3C



S	W	K	Q	D	M	E	R	G	N	P	E	W	A	C	A	S	G	P	M
TCC	TGG	AAG	CAG	GAC	ATG	GAG	CGG	GGG	AAC	CCA	GAG	TGG	GCA	TGT	GCC	AGT	GGC	CCC	ATG
S	R	S	L	R	P	Q	S	R	P	Q	I	I	K	E	V	L	A	V	P
AGC	AGG	AGC	CTT	CGG	CCT	CAG	AGC	CGC	CCG	CAA	ATC	ATT	AAA	GAA	GTC	CTG	GTC	CCC	1747
N	S	I	L	E	L	P	C	P	H	L	S	A	L	A	S	Y	Y	W	S
AAC	TCC	ATC	CTG	GAG	CTC	CCC	TGC	CCC	CAC	CTG	TCA	GCC	TTG	GCC	TCT	TAT	TAT	TGG	AGT
H	G	P	A	A	V	P	E	A	S	S	T	V	Y	N	G	S	L	L	592
CAT	GGC	CCA	GCA	GCA	GTC	CCA	GAA	GCC	TCT	TCC	ACT	GTC	TAC	AAT	GGC	TCC	CTC	TTG	CTG
I	V	Q	D	G	V	G	G	L	Y	Q	C	W	A	T	E	N	G	F	S
ATA	GTG	CAG	GAT	GGA	GTT	GGG	GGT	CTC	TAC	CAG	TGC	TGG	GCA	ACT	GAG	AAT	GGC	TTT	TCA
Y	P	V	I	S	Y	W	V	D	S	Q	D	Q	T	L	A	L	D	P	E
TAC	CCT	GTG	ATC	TCC	TAC	TGG	GTG	GAC	AGC	CAG	GAC	CAG	ACC	CTG	GCC	CTG	GAT	CCT	GAA
L	A	G	I	P	R	E	H	V	K	V	P	L	T	R	V	S	G	G	632
CTG	GCA	GGC	ATC	CCC	CGG	GAG	CAT	GTG	AAG	GTC	CCG	TTG	ACC	AGG	GTC	AGT	GGT	GGG	GCC
A	L	A	A	Q	Q	S	Y	W	P	H	F	V	T	V	T	V	L	F	A
GCC	CTG	GCT	GGC	CAG	CAG	TCC	TAC	TGG	CCC	CAC	TTT	GTC	ACT	GTC	ACT	GTC	CTC	TTT	GCC
L	V	L	S	G	A	L	I	I	V	A	S	P	L	R	A	L	R	A	712
TTA	GTG	CTT	TCA	GGA	GGC	CCC	CTC	ATC	ATC	CTC	ATC	GTC	GGG	GCA	CTC	CGG	GCT	2167	

Fig. 3D



ACTCTAGGCACAGGCCGGGGCTGGGGTGCAGGCACCTGGCCATTGGCTGGGGCCAAAGCACAGCCCTGACTGGCTTAGGAA	2396
TGACAGCGACAAAGACCACCTTCTCCCCCTGAGAGGAGCTTCTGCATCACTGATGACACTCAGCAGGG	2475
TGATGCACAGCAGTCAGCTGGACTTCCCCTATGGACTTCCCCTAACAGCACATGAGCTCTAACAGGGTGGGGCTACCC	2554
CCAGACCTGCTCCTACACTGATAATTGAAGAACCTGGAGAGGGATCCTTCAGTTGGCCATTCCAGGGACCCCTCCAGAAA	2633
CACAGTGTTCAGAGATCCTAAAAAACCTGGCCTGTCCCAGGACCCCTATGGTAATGAACACCCAACATCTAACAAATC	2712
ATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCCTCCAGGGTCA	2791
TGCAGGGATCTGCTCCCTCCCTGCTTACCACTGGCTGACCTCCAGGAAGTCTTCCCTGAAGTCTGACC	2870
ACCTTCTTCAGTTGGCAGACTCTGATCCCTTGCCCTGAGGTAATCTGAGGCTTCT	2949
TCACTCCTTACCCCTAGCTGACCCCTCACCTCTCCCCCTTCCCTTGGATTTCAGAAAACCTGGCTTGTCT	3028
AGAGACTGTTTATTAAAATAAGGCTTAAAAAAGGGGGGGC	3104

Fig. 3E



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Hum.	MALPALGLDPWSLLGLFLFQLLQLLPTTAGGGQQGPMMPRVRYAGDERRALSFFHQKGLQDFDTLLS	10	20	30	40	50	60	70
Mur.	MALPSLGQDSWSLLRVLFFQLFLPSLPPASSGTGGQQGPMMPRVKYHAGDGHRALSFFQQKGLRDFDTLLS	10	20	30	40	50	60	70
Hum.	GDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLY	80	90	100	110	120	130	140
Mur.	DDGNTLYVGARETVIALNIONPGIPRLKNMIPWPASERKKTECAFKKKSNETQCFNFIRVLVSYNVATHLY	80	90	100	110	120	130	140
Hum.	TCGTFAFSPACTFIELDQDSYLLPISEDKVMEKGQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEPILMR	150	160	170	180	190	200	210
Mur.	ACGTFAFSPACTFIELDQDSLLLPLILIDKVMIDKGQSPPLTSTQAVLVDGMLYSGTMNNFLGSEPILMR	150	160	170	180	190	200	210
Hum.	TGSSQPVLKTDNFLRWLHHDASFVAIAIPSTQVVYFFFETASEEFDFFERLHTSRVARVCKNDVGGEKLIQ	220	230	240	250	260	270	280
Mur.	TGSHHPVLKTDIFLRWLHADASFVAIAIPSTQVVYFFFETASEEFDFFEELEYISRVAQVCKNDVGGEKLIQ	220	230	240	250	260	270	280

Fig. 3F



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290	300	310	320	330	340	350
Hum.	KKWTTFLKAQQLLCTQPGQLPENVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF					
Mur.	KKWTTFLKAQQLLCAGQPGQLPFNIIIRHAVLLPADSPSVSRIYAVFTSQWQVGGTRSSAVCAFSLTDIERVF					
290	300	310	320	330	340	350
360	370	380	390	400	410	420
Hum.	KGKYKELNKETSRWTITYRGPETNPRPGSCSVGPSSDKALTFMKDHFILMDEQVVGTPLIVKSGVEYTRLAV					
Mur.	KGKYKELNKETSRWTITYRGSEVSPPRGSCSMGPSSDKALTFMKDHFILMDEHVVGTPLIVKSGVEYTRLAV					
360	370	380	390	400	410	420
430	440	450	460	470	480	490
Hum.	ETAQGLDGSHLVMYLGTTGSLHKAVVSGDSSAHLIVEEIQLFDPPEPVRLNLQLAFTQGAVFVGFSGGVW					
Mur.	ESARGLDGSSHHVVMYLGTTGPLHKAVVPQDSSAYLIVEEIQLSPDSEPVRLNLQLAQGAVFAGFSGGIW					
430	440	450	460	470	480	490
500	510	520	530	540	550	560
Hum.	RVPRANCSVYESCVDCVLARDPHCAWDPESRCTCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRPQS					
Mur.	RVPRANCSVYESCVDCVLARDPHCAWDPESRILCSLLSGST-KPWKQDMERGNPEWVCTRGPMAERSPRRQS					
500	510	520	530	540	550	560

Fig. 3G



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Hum.	RPQIKEVLPNSILELPCPHLSALASYWWSHGPAAVPEASSSTVYNGSLLLIVQDGVGGLYQCWATENG	570	580	590	600	610	620	630
Mur.	PPQLIKEVLTVPNSILELRCPHLSALASYHWSHGRAKISEASATVYNGSLLLQPQDGVGGLYQCVA	560	570	580	590	600	610	620
Hum.	FSYPVISYWVDSQDQLADPELAGTPREHVVKVPLTRSGGAALAAQQSYWPHFVTVTFLFAVLVLSGALLI	640	650	660	670	680	690	700
Mur.	YSYPVVSYWVDSQDQLADPELAGVPRERVQVPLTRVGGASMAAQRSYWPHFLIVTVLLAIIVLLGVLT	630	640	650	660	670	680	690
Hum.	ILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASSDVDADDNNCLGTEVA	710	720	730	740	750	760	
Mur.	LILLASPLGALRARGKVQGCAGMLPPREKAPLSRDQHLLQPSKDHRTSASSDVDADDNNHLGAEVA	700	710	720	730	740	750	760

Fig. 3H



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Hum. GTCGG-AC-CC----- ::::: Mur. CTCGGACGCCCTGGGTAGGGTCTGTA 10 ::::: Mur. CCTACCATTGGCCAGGA 40 Hum. CCTCCCAGCCCTGGC 20 ::::: Mur. CCTACCATTGGCCAGGA 80 Hum. GCTGCCGACG 30 ::::: Mur. ATCACTGCCAC 110 Hum. GCTGCCGACG 50 ::::: Mur. CCTACCATTGGCCAGGA 100 Hum. GCTGCCGACG 70 ::::: Mur. CCTACCATTGGCCAGGA 120 Hum. GCTGCCGACG 90 ::::: Mur. CCTACCATTGGCCAGGA 110 Hum. GCTGCCGACG 130 ::::: Mur. ATCACTGCCAC 150 Hum. GAACTAGGGCACT 180 ::::: Mur. GGGCACAGGGCCCT 210 Hum. GAACGTAGGGCACT 190 ::::: Mur. GGGCACAGGGCCCT 220 Hum. GAACGTAGGGCACT 200 ::::: Mur. GGGCACAGGGCCCT 230 Hum. GAACGTAGGGCACT 210 ::::: Mur. GGGCACAGGGCCCT 240 Hum. GAACGTAGGGCACT 220 ::::: Mur. GGGCACAGGGCCCT 250 Hum. GAACGTAGGGCACT 230 ::::: Mur. GGGCACAGGGCCCT 260 Hum. GAACGTAGGGCACT 240 ::::: Mur. GGGCACAGGGCCCT 270	30 ::::: Mur. CCTACCATTGGCCAGGA 50 ::::: Mur. CCTACCATTGGCCAGGA 70 ::::: Mur. CCTACCATTGGCCAGGA 90 ::::: Mur. CCTACCATTGGCCAGGA 110 ::::: Mur. CCTACCATTGGCCAGGA 130 ::::: Mur. CCTACCATTGGCCAGGA 150 ::::: Mur. CCTACCATTGGCCAGGA 170 ::::: Mur. CCTACCATTGGCCAGGA 180 ::::: Mur. CCTACCATTGGCCAGGA 190 ::::: Mur. CCTACCATTGGCCAGGA 200 ::::: Mur. CCTACCATTGGCCAGGA 220 ::::: Mur. CCTACCATTGGCCAGGA 230 ::::: Mur. CCTACCATTGGCCAGGA 240 ::::: Mur. CCTACCATTGGCCAGGA 250 ::::: Mur. CCTACCATTGGCCAGGA 260 ::::: Mur. CCTACCATTGGCCAGGA 270
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Fig. 3I



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Hum.	ATGAAATACTCTACGTGGGGCTCGAGAACCCATTCTGGATATCCAGGATCCAGGGTCCC	250	260	270	280	290	300	310
Mur.	ATGGCAACACTCTATGTGGGGCTCGAGAGACCGTCCTGGCCTTGAATATCCAGAACCCAGGAATCCC	280	290	300	310	320	330	340
Hum.	CAGGCTAAAGAACATGATAACCGTGGGCCAGCCAGGTGACAGAAAAAGAGTGAATGTGCCCTTAAGAAGAAG	320	330	340	350	360	370	380
Mur.	AAGGCTAAAGAACATGATAACCCCTGGCCAGCCAGGTGAGAGAAAAAGACCGAATGTGCCCTTAAGAAGAAG	350	360	370	380	390	400	410
Hum.	AGCAATGAGACACAGTGTTCAACTCATCCGTGTCTGGTTTACAATGTCACCCATCTTACACCT	390	400	410	420	430	440	450
Mur.	AGCAATGAGACACAGTGTTCAACTCATCGAGTCCTGGTCTCTTACAATGCTACTCACCTCTATGCCT	420	430	440	450	460	470	480
Hum.	GCGGCACCTTCGCCTTCAGCCCTGCTTGACCTCATTGAACCTCAAGATTCTACCTGTTGCCCATCTC	460	470	480	490	500	510	520
Mur.	GTGGGACCTTTGCCTTCAGCCCTGCTGTACCTCATTGAACCTCAAGATTCCACTCCTCCATTGCCCCATCTT	490	500	510	520	530	540	550

Fig. 3J



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Hum.	GGAGACAAGGTCATGGAGGAAAGGCCAAGCCCCCTTGACCCCGCTCACAAAGCATAACG-GCTGTCTT	530	540	550	560	570	580	590
Mur.	GATAGACAAGGTCATGGACGGGAAGGCCAAGCCC-TTTGACCCTGTCACAAGCACACAAGCTGTCTT	560	570	580	590	600	610	620
Hum.	GGTGGATGGGATGGCTCTATTCTGGTACTATGAAACAACTTCCCTGGCAAGTGAGCCCATCCTGATGCCACA	600	610	620	630	640	650	660
Mur.	GGTCGATGGGATGGCTTATTCCGGACCATGAAACAACTTCCCTGGCAAGGCAGGCCATCCTGATGCCACA	630	640	650	660	670	680	690
Hum.	CTGGGATCCCAGCCCTGTCCCTCAAGACCGACAACTTCCGCTGGCTGCATCATGACGCCCTCCTTGTGG	670	680	690	700	710	720	730
Mur.	CTGGGATCCCATCCCTGTTCTCAAGACTGACATCTTACGGCTGGCTGCACGCCGATGCCCTCCTGCG	700	710	720	730	740	750	760
Hum.	CAGCCATCCCTCGACCCAGGTCTACTTCTCGAGGAGACAGCCAGCGAGTTGACTTCTTTGA	740	750	760	770	780	790	800
Mur.	CAGCCATTCCACCCAGGTCTATTCTTCTCGTCTATTGAGGAGACAGCCAGCGAGTTGACTTCTTTGA	770	780	790	800	810	820	830

Fig. 3K



Hum.	GAGGCTCCACACATCGGGTGGCTAGAGTCTGCAGAAATGACGTGGCGGGCAGAAG	810	820	830	840	850	860	870
Mur.
	AGAGCTGTATAATCCAGGGTGGCTCAAGTCTGCAGAAACGACGTGGCGGTGAAAGCTGCTGCAGAAG	840	850	860	870	880	890	900
Hum.	AAGTGGACCACCTTCTGAAAGGCCAGCTGGCTCTGCACCCAGCCGGGCAGCTGCCCTCAACGTCATCC	880	890	900	910	920	930	940
Mur.
	AAGTGGACCACCTTCTCAAAAGCCCAGTTGGCTCTGCCTCAGGCCAGGGCAGCTGCCATTCAACATCATCC	910	920	930	940	950	960	970
Hum.	GCCACGGGGCTGGCTCCCCGCCGATTCTCCACAGCTCCCCACATCTACGCAGTCTCACCTCCCCAGTG	950	960	970	980	990	1000	1010
Mur.
	GCCACGGGGCTGGCTGCCGCCGATTCTCCCTCTGGTTCCCGCATCTACGCAGTCTCACCTCCCCAGTG	980	990	1000	1010	1020	1030	1040
Hum.	GCAGGGTGGGGACCAAGGAGCTGGCTTGTGGCTCTCTGGACATTGAAACGTGTCTTAAG	1020	1030	1040	1050	1060	1070	1080
Mur.
	GCAGGGTGGGGACCAAGGAGCTCAGGCAGTCTGTGGCTTCTCTCACGGACATTGAGCGAGTCTTTAAA	1050	1060	1070	1080	1090	1100	1110

Fig. 3L



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Hum.	GGAAATAACAAAGAGTTGAACAAAGAAACTCACGCTGGACTTATAGGGCCCTGAGACCAACCCCC	1090	1100	1110	1120	1130	1140	1150
Mur.	GGAAAGTACAAGGAGGTGAAACAAGGAGACCTCCCGCTGGACCACTTACCGGGCTCAGAGGTAGCCGA	1120	1130	1140	1150	1160	1170	1180
Hum.	GGCCAGGCAGTTGCTTCAGTGGCCCTCCTGACCTTCATGAAGGACCATTTCCTGAT	1160	1170	1180	1190	1200	1210	1220
Mur.	GGCCAGGCAGTTGCTCCATGGCCCTCCTGACAAAGGCCCTGACCTTCATGAAGGACCATTTCCTGAT	1190	1200	1210	1220	1230	1240	1250
Hum.	GGATGAGCAAAGTGGTGGGACGGCCCTGCTGGTGAATCTGGCGTGGAGTACACGGCTTGAGTGGAG	1230	1240	1250	1260	1270	1280	1290
Mur.	GGATGAGCACAGTGGTAGGAAACACCCCTGCTGGTGAAGTCTGGTGTGGAGTACACAGGGCTTGCTGTGGAG	1260	1270	1280	1290	1300	1310	1320
Hum.	ACAGCCCAGGGCCTTGATGGCACAGCCATCTTGTATGTACCTGGGAACCAACAGGGTCCGCTCCACA	1300	1310	1320	1330	1340	1350	1360
Mur.	TCAGGCTCGGGCCTTGATGGGAGCAGGCCATGTGGTCATGTATCTGGGTACCTCCACGGGTCCCCCTGCA	1330	1340	1350	1360	1370	1380	1390

Fig. 3M



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1370	1380	1390	1400	1410	1420	1430
Hum.	AGGCTGTGGTAAGTGGGACAGCAGTGCTCATCTGGTGGAAAGAGATTCAGCTGTTCCCTGACCCCTGAAACC					
1400	1410	1420	1430	1440	1450	1460
Mur.	AGGCTGTGGTGCCTCAGGACAGCAGTGCTTATCTCGTGGAGGAGATTCAGCTGAGCCCTGACTCTGAGGCC					
1440	1450	1460	1470	1480	1490	1500
Hum.	TGTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTGTAGGCTTCTCAGGAGGGTGTCTGGAGG					
1470	1480	1490	1500	1510	1520	1530
Mur.	TGTTCGAAACCTGCAGCTGGCCCCAGGGTGCAGTGTGCAGGCTTCTGGAGGCATCTGGAGA					
1510	1520	1530	1540	1550	1560	1570
Hum.	GTGCCCCGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCCTGCCGGACCCCACTGTG					
1540	1550	1560	1570	1580	1590	1600
Mur.	GTTCCCAGGGCCAATTGCAGTGTCTACGAGAGCTGTGTGGACTGTGTGCTTGCAGGGACCCCTCACTGTG					
1580	1590	1600	1610	1620	1630	1640
Hum.	CCTGGACCCCTGAGTCCCGAACCTGTTGCCCTCCTGTCTGCCAACCTGAACCTCCTGGAAAGCAGGACAT					
1610	1620	1630	1640	1650	1660	1670
Mur.	CCTGGACCCCTGAGACTCTGCAGCCTTCTGTCTGGCTC-TACCAAGCCT--TGGAAGCAGGACAT					

Fig. 3N



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Hum.	GGAGCGGGAAACCCAGAGTGGGCATGTGCCAGTCAGTGGCCCCATGAGCAGGAGCCCTCGGCCCTCAGAGCCGC	1650	1660	1670	1680	1690	1700	1710
Mur.	GGAACGGCAACCCGGAGTGGGTATGCACCCGTGGCCCATGGCCAGGAGCCCCGGCGTCAGAGCCCC	1680	1690	1700	1710	1720	1730	1740
Hum.	CCGCAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCCTGCCACCTGTCAG	1720	1730	1740	1750	1760	1770	1780
Mur.	CCTCAACTAATTAAAGAAGTCCTGACAGTCCCCAACTCCATCCTGGAGCTGGCTGCCACCTGTCAG	1750	1760	1770	1780	1790	1800	1810
Hum.	CCTTGGCCTCTTATTGGAGTCATGGCCAGCAGTCCCAGAAGCCTCTTCCACTGTCATAATGG	1790	1800	1810	1820	1830	1840	1850
Mur.	CACTGGCCTTACCACTGGAGTCATGGCCAGCCAAAATCTCAGAAGCCTCTGCTACCGTCTACAATGG	1820	1830	1840	1850	1860	1870	1880
Hum.	CTCCCTCTTGCTGATAGTCAGGATGGAGTTGGGGTCTCTACCAGTGCTGGCAACTGAGAATGGCTTT	1860	1870	1880	1890	1900	1910	1920
Mur.	CTCCCTCTTGCTGCCAGGATGGTGTGGCGACTTACCACTGGCTGGCGACTGAGAACGGCTAC	1890	1900	1910	1920	1930	1940	1950

Fig. 30



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Hum.	TCATACCCCTGTGATCCTACTGGTGGACAGGCCAGGACCAGACAGCCCTGGCATCCTGAGACTGGCAG	1930	1940	1950	1960	1970	1980	1990
Mur.	TCATACCCCTGTGCTCCTATTGGTAGACAGCCAGGACCAGGCCCTGGCGCTGGACCCCTGAGCTGGGG	1960	1970	1980	1990	2000	2010	2020
		2000	2010	2020	2030	2040	2050	2060
Hum.	GCATCCCCGGGAGCATGTGAAGGTTCCCGTTGACCAGGGTCAGTGGTGGGGCGCCCTGGCTGCCAGCA	2030	2040	2050	2060	2070	2080	2090
Mur.	GCGTTCCCCCGTGAGCGTGTGCAAGGTCCCGTGTGACCAAGGGTCCGGAGGGGGAGCTCCATGGCTGCCAGCG	2040	2050	2060	2070	2080	2090	2100
		2070	2080	2090	2100	2110	2120	2130
Hum.	GTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTTTGCCTTAGTGCCTTCAGGAGCCCTCATCATC	2100	2110	2120	2130	2140	2150	2160
Mur.	GTCCTACTGGCCCCATTTCATCGTTACCGTGTGCTCCTGGCCATCGTGGAGTGCTCACTCTC	2110	2120	2130	2140	2150	2160	2170
		2140	2150	2160	2170	2180	2190	2200
Hum.	CTCGTGGCCCTCCCCATTGAGAGCAC'TCCGGGCTCGGGCAAGGTTCAAGGGCTGTGAGACCCCTGGCCCTG	2170	2180	2190	2200	2210	2220	2230
Mur.	CTCCTCGCTTCCCCACTGGGGCGCTGGGGCTAAGGTTCAAGGGCTGTGGGATGCTGGCCCCCA	2180	2190	2200	2210	2220	2230	2240

Fig. 3P



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Hum.	GGGAGAACCCCGTTAAGCAGAGCAACACCTCCAGTCTCCAAAGGAATGCCAGCTGCCAGTGA	2210	2220	2230	2240	2250	2260	2270
Mur.	GGGAAAAGGCTCACTGAGCAGGGACCAGCACCCTCCAGCCCTCCAAGGACCAACAGGACCTCTGCCAGTGA	2240	2250	2260	2270	2280	2290	2300
Hum.	TGTGGACGGCTGACAACAAACTGCCATTAGGCACITGAGGTAGCCTAAACTCTAGGCACAGG-CGGGGCTG--C	2280	2290	2300	2310	2320	2330	2340
Mur.	CGTAGATGCCGACAAACACCATTCTGGGCCGAAGTGGCTTAACAA-GGGACACAGATCCGCAGCTGAGC	2310	2320	2330	2340	2350	2360	2370
Hum.	GGTCAGGCACCTGGCCATGCTGGCTGGGGCCAAAGCACAGCCTGACTAGGATGACAGCAGCACAAA	2350	2360	2370	2380	2390	2400	2410
Mur.	AGAGCAAGCCACTGGCCCTTGGCTATGC---CAGGCACAG-----TGCCACTCT--	2380	2390	2400	2410	2420		
Hum.	AGACCACCTTTCTCCCTGAGAGGAGCTCTGCATCACTGATGACACTCAGCAGGGTGTGATGC	2420	2430	2440	2450	2460	2470	2480
Mur.	-GACCA-----GGGTAGGAG--GCT-CT-GCTCA-C-TACAG-----C	2430	2440	2450				

Fig. 30



2490	2500	2510	2520	2530	2540	2550
Hum.	ACAGCAGTCCTG-CCTCCCCCTATGGACTCCCTTCTACCAAGCACATGAGCTCTAACAGGGTGGGGCT					
::	:::	:::	:::	:::	:::	:::
Mur.	ACC-CAGTAGGTCCCTCCCCCTGTGGACTCTCTGC-AAGCACATT-----GGGCT					
2470	2480	2490	2500	2510		
2560	2570	2580	2590	2600	2610	
Hum.	ACCCCCAGACCTGCTCCCTACACTGATA-TTGAAGAACCTGGAGAGGATCCTTCAGTTCTGCCATTCCAG					
::	:::	:::	:::	:::	:::	:::
Mur.	GTCTCCATACCTGTACTTGTGCTGTGACAGGAAGGCCAGAC-AGGTTCCTTGATTGACCCAA					
2520	2530	2540	2550	2560	2570	2580
2620	2630	2640	2650	2660	2670	2680
Hum.	GGACCCCT-CCAGAAACACA-GTGTTCAAAGAGATCCCTAAAAAACCTGCCTGCCAGGACCCATTGGTA					
:::	:::	:::	:::	:::	:::	:::
Mur.	GAGCCCTGCCATGTAACAAACAGTGCTCCAGGAGA-CCATGAAAGGTGGCTGGCT-GGGATTCTGTGGTG					
2590	2600	2610	2620	2630	2640	2650
2690	2700	2710	2720	2730	2740	2750
Hum.	ATGAAACACCAACATCTAACAAATCATATGCTAA-CATGC---CAC---TCCTGGAAACT-CCACTCTGAA					
:::	:::	:::	:::	:::	:::	:::
Mur.	ACAAAC-CTAACGATCCGAGCAAGCTGGGCTATTCCCTGCACAAACTCCATCCTGAACGCTGTCACTCTAGA					
2660	2670	2680	2690	2700	2710	2720

Fig. 3R



Hum.	-----GCTGCCGCTTTGGACACCAACACTCCCTTCT-CCCAGG-GTCATGCAGGGATCTGCTCCCTCCTGC	2760	2770	2780	2790	2800	2810		
Mur.	::::: : :: :	2730	AGCAGCTGCTGCTTGAACACCAGCCCACCCCTCCCAAGAGTCTATGGAGTTGGC-CCCTTGTTG	2740	2750	2760	2770	2780	2790
Hum.	TTCCTTACCACTCGTGCACCGCTGACTCCCAGGAAGTCTTCCCTGAAGTCTGACCACCTTTCTTCTTGC	2820	2830	2840	2850	2860	2870	2880	
Mur.	::::: : :: :	2800	TTCCCTTACCACTCGGCCATACTGTT---GGAAAGTCATCTCTGAAGTCTAACCAACCCTCCCTCTGG	2810	2820	2830	2840	2850	
Hum.	TTCAGTTGGGCAGACTCTGATCCCT---TCTGCCCTGGCAGAATGGCAGGGTAATCTGAGCCTTCTC	2890	2900	2910	2920	2930	2940	2950	
Mur.	::::: : :: :	2860	TTCAGTTGGACAGATTGTATTATTGTCTGCCCTGGCTAGAAATGGGGCATAATCTGAGCCTTGTTC	2870	2880	2890	2900	2910	
Hum.	ACTCCTTACCC---TAGCTGACCCCTCACCTCTCCC---CCTCCCTTTGTTCCCTGGATTCAAGA	2960	2970	2980	2990	3000	3010		
Mur.	::::: : :: :	2930	---CCTTGTCCAGTGGCTGACCC-TTGACCTCTTCCCTCC---TCCCTTGTGTTGGATTCAAGA	2940	2950	2960	2970	2980	

Fig. 3S



Hum.	AAACTGCTTGTCAAGACTGTTATTTTATTAAAAATATAAGGCTTAA	3080
:.....:.....:.....:.....:.....:.....:.....:.....::.....:.....:.....:.....:.....:.....:.....:.....:
Mur.	AAACTGCTTGTCAAGACAATTATTTTATTAAAA-	3070
:.....:.....:.....:.....:.....:.....:.....:.....::.....:.....:.....:.....:.....:.....:.....:.....:
	- - - - - AGATATAA	3060
	- - - - -	3050
Hum.	AAACTGCTTGTCAAGACTGTTATTTTATTAAAAATATAAGGCTTAA	3040
:.....:.....:.....:.....:.....:.....:.....:.....::.....:.....:.....:.....:.....:.....:.....:.....:
Mur.	AAACTGCTTGTCAAGACAATTATTTTATTAAAA-	3030
:.....:.....:.....:.....:.....:.....:.....:.....::.....:.....:.....:.....:.....:.....:.....:.....:
	- - - - - AGATATAA	3020
	- - - - -	3010
Hum.	AAACTGCTTGTCAAGACTGTTATTTTATTAAAAATATAAGGCTTAA	3000
:.....:.....:.....:.....:.....:.....:.....:.....::.....:.....:.....:.....:.....:.....:.....:.....:
Mur.	AAACTGCTTGTCAAGACAATTATTTTATTAAAA-	3000
:.....:.....:.....:.....:.....:.....:.....:.....::.....:.....:.....:.....:.....:.....:.....:.....:
	- - - - - AGATATAA	3000
	- - - - -	3000
Hum.	AAACTGCTTGTCAAGACTGTTATTTTATTAAAAATATAAGGCTTAA	3090
:.....:.....:.....:.....:.....:.....:.....:.....::.....:.....:.....:.....:.....:.....:.....:.....:
Mur.	AAACTGCTTGTCAAGACAATTATTTTATTAAAA-	3100
:.....:.....:.....:.....:.....:.....:.....:.....::.....:.....:.....:.....:.....:.....:.....:.....:
	- - - - - AGATATAA	3100
	- - - - -	3100

Fig. 3T



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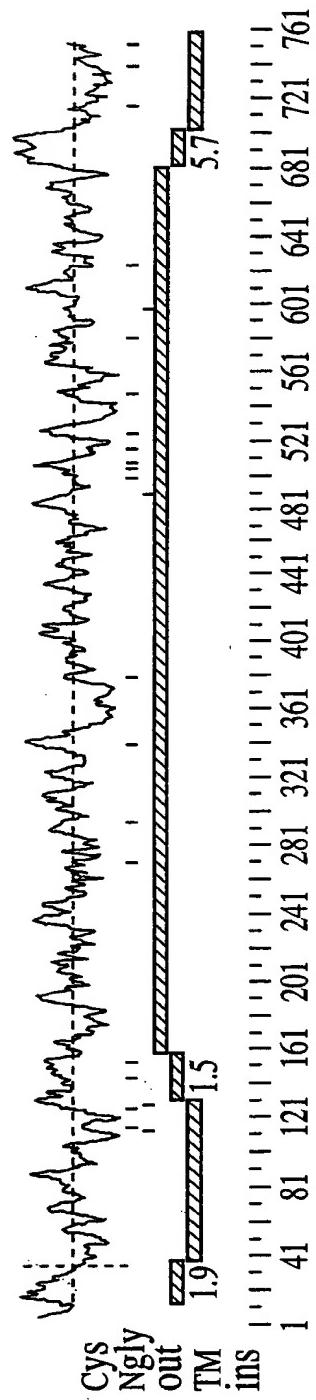


Fig. 3U



GTCGACCCACGGCTCGGGACGGCTCGGGCTCCGGCTGGAGGGACGGCTGGCTCTGCAGTCTGCCCGCCCCGGCGGGCCAGTC
 M R R Q P A 6
 GCGAAGCGGCCTGCGACCCGGTCCGGCTGGAGGGACGGAGGCC ATG AGG CGC CAG CCT GCG 152
 K V A A L L G L L E C T E A K K H C 26
 AAG GTG GCG GCG CTG CTC GGG CTG CTC ACA GAA GCC AAA AAG CAT TGC 212
 W Y F E G L Y P T Y Y I C R S Y E D C C 46
 TGG TAT TTC GAA GGA CTC TAT CCA ACC TAT TAT ATA TGC CGC TCC TAC GAG GAC TGC TGT 272
 G S R C C V R A L S I Q R L W Y F W F L 66
 GGC TCC AGG TGC TGT GTG CGG GCC CTC TCC ATA CAG AGG CTG TGG TAC TTC TGG TTC CTT 332 / 95
 L M M G V I F C C G A G F F I R R M Y 86
 CTG ATG ATG GGC GTG CTT TTC TGC TGC GGA GCC GGC TTC TTC ATC CGG AGG CGC ATG TAC 392
 P P P L I E P A F N V S Y T R Q P P N 106
 CCC CCG CTG ATC GAG GAG CCA GCC TTC AAT GTG TCC TAC ACC AGG CAG CCC CCA AAT 452
 P G P G A Q P G P Y Y T D P G G P G 126
 CCC GGC CCA GGA GCC CAG CAG CCG CCG CCC TAT TAC ACT GAC CCA GGA CCG GGG 512
 M N P V G N S M A M A F Q V P P N S P Q 146
 ATG AAC CCT GTC GGG AAT TCC ATG GCA ATG GCT TTC CAG GTC CCA CCC AAC TCA CCC CAG 572

Fig. 4A



G S V A C P P P P N T P P P Y E 166
 GGG AGT GTG GCC TGC CCG CCC CCT CCA GCC TAC TGC AAC ACG CCT CCG CCC CCG TAC GAA 632
 Q V V K A K *
 CAG GTA GTG AAG GCC AAG TAG

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TGGGGTCCCCACGTGCAAGAGGAGACAGGAGAGGAGGCTTCCCTGGCCTTCTGTCTCGTTGATGTTCACTTCAG
 GAACGGGCTCGTGGCTAAGGCAGTTCCCTGATATCCTCACAGCAAGCACAGCTCTTCAGGCTTCCCATGG 811
 AGTACAATATGAACACTACACTTTGTCCTCTGTTGCTCACATGGTAGCTGACGGCAGTCTGACGGCTCTGCTCTGCT
 GGTGACAGTCCCCGAGGGCTGACGTCCCTAACGGTGGCATGACAGGAGAGACTGAGAGGAAAGAGCAG 969
 TGCTGGAGGTGCAGGTGCAGGTGGCATGTTAGAGGGCTAGGGAGGCTAGGGAGGGTACGGAGGAGGCTAGGG
 AAGGCCCATGCCGGGGCTCAGCCGATGAAGCAGCAGCCGACTGAGCTGAGCCAGGAGGCTCAGGAGGAGGCT
 CCTCTCGTCAGCCTCCCTCTCCAGAAAGCTGTTGGAGAGACATTAGGAGAGGAGGAGGAGGAGGAGGAGG
 CTGTTCATATCCTAAAGATAAGCTTCTCTGCACCCGCCAGGGAAAGGGTAGCAGCTGCAGGCTCAGGGAGG
 CTAGAATCAGGGCTTGCCCTGGAGGCTGACAGTGATCTGACATCCACTAAGCAAATTATTAAATTCA
 CTTCCCTGCCCAACTGAGACATTGCAATTGGTCTGATTTGGAGAAAGGAACTGTTACCCCATTTTTG 1443
 GTGTGTTATGGAAGTGCATGTAAGGGCTCTGGCCCTTGAATCAGACTGGGTGTGTGTCTCCCTGGACAT
 CCTCTCCAGGGCATTCTCAGGGCCGGGGTCTCCCTCAGGCAAGCTCCAGTGGGGTCTGAAGGGTGTCAA
 ACGGGGCACATCTGGCTGGGAAGTCACATGGACTCTCCAGGGAGAGGAGACCAGGCTGAGGGTCT
 GTTGGGTCTAAGGGGTCCAAGGAGGGAGCTTGTGCTGGGAAAGACAGGGAAAGTACTGACTCAAC
 TGCACTGACCATGTTGTCATAATTAGAATAAGAAGAAGTGGTGGAAATGCACATTCTGGGATAGGAAT
 CCCCAAGGATCTCACAGGTAGTGTCTGAGTAGTGTGCTGGGGAGCTAGGGCTAGTCCGGCGCATAGTT
 TGTGTGAAACGCTGACCTGTCCCTGTGTGCTAAGAGCTATGCAGCTTAGCTGAGGGCCTAGATTACT
 CACGGGGAAATGAGGGGGTGTCTTAAATGAACATACTAGAGCCCTTGGAGAAATTGTTACTCATGA
 AGCATCAAGACATCTCATGGAAGTGGATACGGGAGTGGCATTTGGCCATGCTTCACTTGGAGATT
 732 890 1048 1206 1285 1364 1522 1601 1680 1759 1838 1917 1996 2075 2154

Fig. 4B



AACCTCCTGGGAATTGTGGAGACACTTGGGAACAAACAGACACCCCTGGGAATGCAAGCACAGTGCTG
 CCACCAAGTGTCTGACCAACCCCTGGTCACTGACTGCCAGCGTGGTACCTCCCATTGCTGCAGGCCCTCCATCTAAA 2233
 TGAGACAAACAAAGCACAACTGTTCACTGTTAATGTCTTTAATTTGTAATGAAAAGCACACTGCGTGGTCCAACACTCCTCTGGCAGGTCA 2312
 TTTGTTGCATTTCATTTGTTAATGTCTTTGTTGACTAAATTTCGTTGCTTTGATAAGCAAATTATGTTAAGAGACAGTGATGGCTAG 2391
 ATAGGCACCCAAAAGTCCCGTGAACATTTGGTGGAGACAGAGTTGTTGAGACAGAGTTGTTGAAACTTGGTTAGAATTGGCTACTGT 2470
 GCTCAACAATTGTATTCCCATGTTGCTTCCACTGGTGAACATTGGCATTGGCATTGGTGGATGGTGG 2549
 GAACGGCTGATCCTGCATATGGAAGTCCACTGGTGAACATTGGCATTGGTGGATGGTGG 2628
 TTGTGCCCACTTCCTGGAGTGAGACAGCTCCTGGTGTAGAATTCCCGAGCGTCCGGTCAAGAGTAAACTTGAAG 2707
 CAGATCTGTGCATGCTTTCCCTCTGCAACAATTGGCTCGTTCTCTTTGATAGGATCCTGTTCT 2786
 ATGTTGCAAAATAAAATAATTGGCAAAAAAAATGGCAAAAAAAATGGCAAAAAAAATGGCAAAAAAAATGGCAAAAAAAATGGCAAAAAAA 2865
 AAAAAAAAGGGCGGCCGC 2944
 AAACCCACGGTCCGGCCGGCGTCTGGCGCTTCAGCTCGTATCCCCGGAGTCCACCCGGCTCCGGGT 2964

Fig. 4C

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GTCGACCCACGGTCCGGCCGGCGTCTGGCGCTTCAGCTCGTATCCCCGGAGTCCACCCGGCTCCGGGT 79
 GCGGACTGGCCCTGAGCTGGCCGTACAGCCGGCTTGGACGGTCTGGAGGCC ATG GGC CGC CGG CTC 151
 G R V A A L L G L V E C T E A K K H 25
 GGC AGG GTG GCG GCG CTC GTC GGG CTG CTA GTG GAG TGC ACT GAG GCC AAA CAT 211

Fig. 4D



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C	W	Y	F	E	G	L	Y	P	T	Y	Y	I	C	R	S	Y	E	D	C	45	
TGC	TGG	TAT	TTT	GAA	GGA	CTC	TAT	CCC	ACA	TAC	TAT	ATA	TGC	CGT	TCC	TAT	GAA	GAC	TGC	271	
C	G	S	R	C	C	V	R	A	L	S	I	Q	R	L	W	Y	F	W	F	65	
TGT	GGC	TCC	AGG	TGC	TGT	GTG	AGG	GCC	CTT	TCC	ATA	CAG	AGG	CTG	TGG	TAT	TTT	TGG	TTC	331	
L	L	M	M	G	V	L	F	C	C	G	A	G	F	F	I	R	R	R	M	85	
CTG	CTG	ATG	ATG	GGT	GGT	GTG	CTG	TTC	TGC	TGT	GGT	GCC	GGT	TTC	TTC	ATT	CGC	CGG	CGC	ATG	391
Y	P	P	P	L	I	E	E	P	T	F	N	V	S	Y	T	R	Q	P	P	105	
TAT	CCG	CCA	CCA	CTC	ATT	GAG	GAG	CCC	ACA	TTC	AAT	GTG	TCC	TAT	ACC	AGG	CAG	CCA	CCA	451	
N	P	A	P	G	A	Q	Q	M	G	P	P	Y	Y	T	D	P	G	G	P	125	
AAT	CCT	GCT	CCA	GGA	GCA	CAG	CAA	ATG	GGA	CCG	CCA	TAT	TAC	ACC	GAC	CCT	GGA	GGA	CCC	511	
G	M	N	P	V	G	N	T	M	A	M	A	F	Q	V	Q	P	N	S	P	145	
GGG	ATG	AAT	CCT	GTT	GGC	AAT	ACC	ATG	GCT	ATG	GCT	TTC	CAG	GTC	CAG	CCC	AAT	TCA	CCT	571	
H	G	G	T	T	Y	P	P	P	S	Y	C	N	T	P	P	P	P	Y	165		
CAC	GGA	GGC	ACA	ACT	TAC	CCA	CCC	CCT	CCT	TAC	TAC	TGC	AAC	ACG	CCT	CCA	CCC	CCC	TAT	631	
E	Q	V	V	K	D	K	*													173	
GAA	CAG	GTG	GTG	AAG	GAC	AAG	TAG													655	

CAAGATGCTACATCAAAGGCAAAGAGGATGGACAGGGCCCTTTGTTACCCATCCCTACCGATACTTGCTGATAG 734

Fig. 4E



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GGTGGTCCAAGGAAACTTGGATATTCTCAAAGCAAGCCCCAGCTCTTTCAAGTCTTGTGGAGGACATTGAATC 813
 CACACTGTCTCCTCTGTTGCTCTGTGATGAGTTCTGGAGGAGGGCTAAGGGAAAGGAAGGCATAGCCTGTGAGGGTT 892
 GATATTCCTAGGGTGTCCAGGGTAGATCCTCGGGAGAGGGCTAAGGGAAAGGAAGGCATAGCCTGTGTTAGGGGG 971
 CAGATAAAGTGGTCAGGCTGAGATAAGACTCACATGATGCCAGTAGTGGCAGTGAACTTCGAAGAGACACTATCCACCA 1050
 TCCCAGCCCCATTCTCCCTAATAGAAAGCTGGGGCTGTTGATGCTTGGGTCTCCACTCACATTGAAATAAG 1129
 GCTTTCCTCTGCCAGGAATAGGAAAGACCCAAAGTACATATTGCTTCCACTTAAAATGAGGGTCAAGAACCGGCTCAG 1208
 TTGGACATCTATAGTTAAATAAGGGCAATTAGAGGGAAATTCTTAAGTTAGGGAAATTCTCTAAATGGAGACATT 1287
 GCGTTTTATGAAATCATCGTCTGGCTTCTACTCAGAGGGCTCCAACACCCCTTTAGTTGAGATGACCCCTTGAGGAGGACAGCCAAAG 1366
 AGTGAACACTGGGCACTATAGAGCTGAGGGTAGTTGAGTTGAGCTGATGACATGACCCCTTGAGGAGGAAAGGGAG 1445
 TTATGGGCACTATAGAGCTGAGGGCACATTAGGGCGGACATTAGGGCGGTTAGTTGAGTTGAGGAGGAGGGCTGACATTGACAT 1524
 AAACTCAGCAAAGCAAGCAGCATGGCTAGGGCTAGGGTTAGGAGTTAGGAGCTAGGGTTATGTGATGCCAAGAGATGTGCTGGCCTCA 1603
 GAAGAGGGGACGTTGTGGATAGAGCCGTGAAAACCTACTTACCTAGGCTCATCCATAGATTACAAGTGTGGAGTTAACAGTAAGAAAG 1682
 TGTTAGTTAGAGATGCCATTCCAGGGTAGGAAATCAGAGCTCACAGCTCATCCATAGATTACAAGTGTGGAGTTAACAGTA 1761
 TGGAGTTCTTCCCTTGCGTAGTTAGTCACGGTGTGATGTTAGGAGCTTGTGACTTAAGAGCAA 1840
 GGAAGTTAGCTAAGATGCTAGATTATTATGTTAGTGGGGAGTTGAGGAGGGCTGCAAGGAAGGGCTGACATTG 1919
 TAAATGAGAAAATCAGAGCCATTGATAAAACTGTTACTTGTGGATCAGGCATCCAAAGTGTCTCTTGAGTGGACATT 1998
 GAGTATTCTTACCACTACAGACCCAGGGCATGGGTCAATTGGGTATTATGAGGTAGAGGTTCAG 2077
 GAATCGACAGTAGCTGTGGGGCTTAGTTAAGGGACTGAAAGCATAGGACTGGTAGACAGTTCATAGGAAACTGGGG 2156
 GGAAGGAATGGATAACCTTAAAGACAGTTGTGGATGCCACCCATCATGGACCCCTGTGTCTGTGGC 2235
 TTCCTGTCACTGGATCCAGTACCCCTCCATGCTTGGGTCTTACATAAGACAAACAAAGCACAAATGTCGTGTT 2314
 TACAATCAAGACGGACTACATGGTCCAAACATTGCTTCTTACACTTGTGGCTTAACTCCATTTCCTCCCGTT 2393
 CCTTTTAAATCAAGAACAGCTCAGAGCTGGCCCTGGGATTGCATCAGGGCTGATCAAGGCATTCAAGGCTCAAGCAATTGCTAAGGCT 2472
 CATGACTAAATCTTATCTTTGATAGCAAATCCTTTAAGAAAAGTGAACAAATGCTAAGGCTCAACTGACAATGACGTCAACACTGACAT 2551
 CAATGTCGTGTAAGGTAATTTGTTGCCATTGAGCCCCACATTGAAATTCCCTCTGACGCTCAACACTGACAATGAC 2630
 ATGGAAATTGCACTCTGGTATATGTCCTGAGCATCCCCAGCATCCCTGGTTATGTTGGTGGAGTAAGGCTCACCCCTTCAGC 2709

Fig. 4F



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AGCTCTACTTCTGTGCTGAGGTCCCTGTAGAGCCGGCTTGGGCACAGACATGAGGCAGACTTGTGCATGCTCTTC 2788
TTGGCAACACTTGGCTCATATTCTTGTCTCTGTATAGAGTCCTATGTATTAAATAAAAGTG 2867
AATTAGTCAAAAAAAGGGCGGCCGC 2915

Fig. 4G

Hum.	MRRQPAKVAALLGLLLECTEAKKHCKWYFEGGLYPTYYICRSYEDCCGSRCVRA LSIQRLWYFWFLLMMG	10	20	30	40	50	60	70
Mur.	MGRRLGRVAALLGLLVECTEAKKHCKWYFEGGLYPTYYICRSYEDCCGSRCVRA LSIQRLWYFWFLLMMG	10	20	30	40	50	60	70
Hum.	VLFCCGAGFFIRRRMYPPLIEEPAFNVSYTROPPNPGP GAQQPGPPYYTDPGGPMNPVGNSMAMAFQV	80	90	100	110	120	130	140
Mur.	VLFCCGAGFFIRRRMYPPLIEEPFTNVSYTRQPPNPAPGA QQMGPPYYTDPGGPMNPVGNTMAMAFQV	80	90	100	110	120	130	140
Hum.	PPNSPQGSVACPPPAYCNTPPPYEQVVVKAK	150	160	170				
Mur.	QPNSPHGGTTYPFFFFSYCNTPPPYEQVVVKDK	150	160	170				

Fig. 4H



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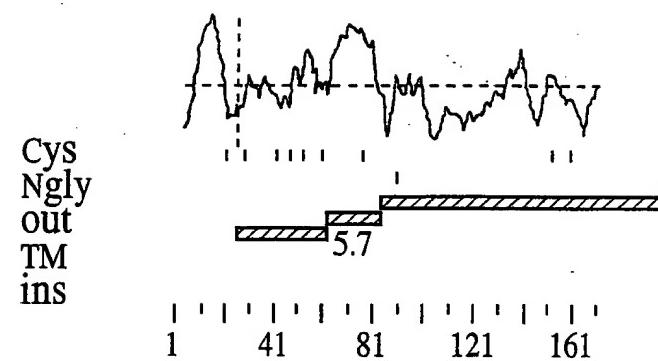


Fig. 4I

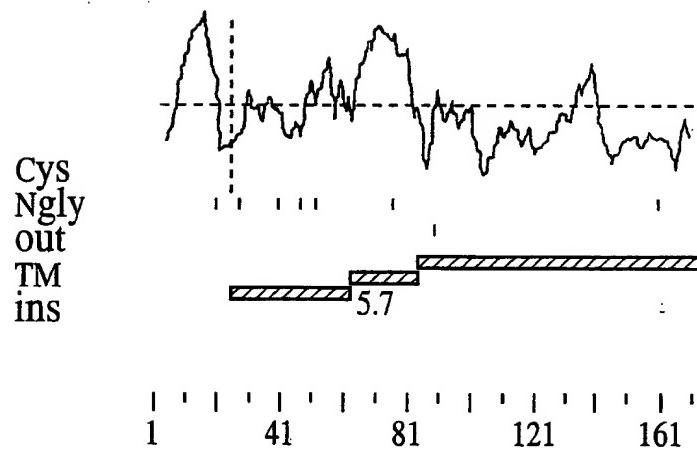


Fig. 4J



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			M	C	T	K	T	I	6											
TCAAGAAAGCCCCAGCACAGCAGAAGATCAGCTGGATCTAGCTCCTGCAGGAG ATG TGT ACA AAG ACA ATC									150											
P	V	L	W	G	C	F	L	W	N	L	Y	V	S	S	Q	T	I	26		
CCA	GTC	CTC	TGG	GGA	TGT	TTC	CTC	CTG	TGG	AAT	CTC	TAT	GTC	TCA	TCC	TCT	CAG	ACC	ATT	210
Y	P	G	I	K	A	R	I	T	Q	R	A	L	D	Y	G	V	Q	A	G	46
TAC	CCT	GGA	ATC	AAG	GCA	AGG	ATT	ACT	CAG	AGG	GCA	CTT	GAC	TAT	GGT	GTT	CAA	GCT	GGA	270
M	K	M	I	E	Q	M	L	K	E	K	K	L	P	D	L	S	G	S	E	66
ATG	AAG	ATG	ATT	GAG	CAA	ATG	CTA	AAA	GAA	AAG	AAA	CTC	CCA	GAT	TTA	AGC	GGT	TCT	GAG	330
S	L	E	F	L	K	V	D	Y	V	N	Y	N	F	S	N	I	K	I	S	86
TCT	CTT	GAA	TTT	CTA	AAA	GTT	GAT	TAT	GTA	AAC	TAC	AAT	TTT	TCA	AAT	ATA	AAA	ATC	AGT	390
A	F	S	F	P	N	T	S	L	A	F	V	P	G	V	G	I	K	A	L	106
GCC	TTT	TCA	TTT	CCA	AAT	ACC	TCA	TTG	GCT	TTT	GTG	CCT	GGG	GTG	GGA	ATC	AAA	GCG	CTA	450
T	N	H	G	T	A	N	I	S	T	D	W	G	F	E	S	P	L	F	V	126
ACC	AAC	CAT	GGC	ACT	GCC	AAC	ATC	AGC	ACA	GAC	TGG	GGG	TTC	GAG	TCT	CCA	CTT	TTT	GTT	510
L	Y	N	S	F	A	E	P	M	E	K	P	I	L	K	N	L	N	E	M	146
CTG	TAT	AAC	TCC	TTT	GCT	GAG	CCC	ATG	GAG	AAA	CCC	ATT	TTA	AAG	AAC	TTA	AAT	GAA	ATG	570

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Fig. 5A



L	C	P	I	I	A	S	E	V	K	A	L	N	A	N	L	S	T	L	E	166
CTC	TGT	CCC	ATT	ATT	GCA	AGT	GAA	GTC	AAA	GCG	CTA	AAT	GCC	AAC	CTC	AGC	ACA	CTG	GAG	630
V	L	T	K	I	D	N	Y	T	L	L	D	Y	S	L	I	S	S	P	E	186
GTT	TTA	ACC	AAG	ATT	GAC	AAC	TAC	ACT	CTG	CTG	GAT	TAC	TCC	CTA	ATC	AGT	TCT	CCA	GAA	690
I	T	E	N	Y	L	D	L	N	L	K	G	V	F	Y	P	L	E	N	L	206
ATT	ACT	GAG	AAC	TAC	CTT	GAC	CTG	AAC	TTG	AAG	GGT	GTA	TTC	TAC	CCA	CTG	GAA	AAC	CTC	750
T	D	P	P	F	S	P	V	P	F	V	L	P	E	R	S	N	S	M	L	226
ACC	GAC	CCC	CCC	TTC	TCA	CCA	GTT	CCT	TTT	GTG	CTC	CCA	GAA	CGC	AGC	AAC	TCC	ATG	CTC	810
Y	I	G	I	A	E	Y	F	F	K	S	A	S	E	A	H	F	T	A	G	246
TAC	ATT	GGA	ATC	GCC	GAG	TAT	TTC	TTT	AAA	TCT	GCG	TCC	TTT	GCT	CAT	TTC	ACA	GCT	GGG	870
V	F	N	L	T	L	S	T	E	E	I	S	N	H	F	V	Q	N	S	Q	266
GTT	TTC	AAT	CTC	ACT	CTC	TCC	ACC	GAA	GAG	ATT	TCC	AAC	CAT	TTT	GTT	CAA	AAC	TCT	CAA	930
G	L	G	N	V	L	S	R	I	A	E	I	Y	I	L	S	Q	P	F	M	286
GGC	CTT	GGC	AAC	GTG	CTC	TCC	CGG	ATT	GCA	GAG	ATC	TAC	TTG	TCC	CAG	CCC	TTC	ATG	990	
V	R	I	M	A	T	E	P	P	I	I	N	L	Q	P	G	N	E	T	L	306
GTG	AGG	ATC	ATG	GCC	ACA	GAG	CCC	ATA	ATC	AAT	CTA	CAA	GGC	AAT	TTC	ACC	CTG	1050		
D	I	P	A	S	I	M	M	L	T	Q	P	K	N	S	T	V	E	T	I	326
GAC	ATC	CCT	GCC	TCC	ATC	ATG	ATG	CTC	ACC	ACC	CCC	AAG	AAC	TCC	ACA	GTT	GAA	ACC	ATC	1110

Fig. 5B



V	S	M	D	F	V	A	S	T	S	V	G	L	V	I	L	G	Q	R	L	346
GTT	TCC	ATG	GAC	TTC	GTT	GCT	AGT	ACC	AGT	ACC	GGT	CTG	GTG	ATT	TTG	GGA	CAA	AGA	CTG	1170
V	C	S	L	S	L	N	R	F	R	L	A	L	P	E	S	N	R	S	N	366
GTC	TGC	TCC	TTG	TCT	CTG	AAC	AGA	TTC	CGC	CTT	GCT	TTG	CCA	GAG	TCC	AAT	CGC	AGC	AAC	1230
I	E	V	L	R	F	E	N	I	L	S	S	I	I	H	F	G	V	L	P	386
ATT	GAG	GTC	TTG	AGG	TTT	GAA	AAT	ATT	CTA	TCG	TCC	ATT	CTT	CAC	TTT	GGA	GTC	CTC	CCA	1290
L	A	N	A	K	L	Q	Q	G	F	P	L	P	N	P	H	K	F	L	F	406
CTG	GCC	AAT	GCA	AAA	TTG	CAG	CAA	GGA	TTT	CCT	CTG	CCC	AAT	CCA	CAC	AAA	TTC	TTA	TTC	1350
V	N	S	D	I	E	V	L	E	G	F	L	L	I	S	T	D	L	R	Y	426
GTC	AAT	TCA	GAT	ATT	GAA	GTT	CTT	GAG	GGT	TTC	CTT	TTG	ATT	TCC	ACC	GAC	CTG	AAG	TAT	1410
E	T	S	S	K	Q	Q	P	S	F	H	V	W	E	G	L	N	L	I	S	446
GAA	ACA	TCC	TCA	AAG	CAG	CAG	CCA	AGT	TTC	CAC	GTA	TGG	GAA	GGT	CTG	AAC	CTG	ATA	AGC	1470
R	Q	W	R	G	K	S	A	P	*											456
AGA	CAG	TGG	AGG	GGG	AAG	TCA	GCC	CCT	TGA											1500

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TTGCCGGTTGCAATTCCCCAGGAAGTAAATGGTCCCTAATCCTACAACTACTGTAAACCCAGAAGGGAAAGACAGT 1579
 ACACACTGGAAATTGTAAGCCCCCTTGAAATTGCTTAGGCAGAAAGTTTCTTTAAGCCTTCAGGAACCCAGAATAA 1658
 GGCAGACTCTGTTAAGGGATAATAGAGGTGCTGAATGTGAGTGTCTGATGCATGCTGCGTGTCTGTGTTATGTTTG 1737
 TTGTTTGGGGCAAGAAGATTCTAGGACAAGAGCTAGGCATGTACTTCTGACCAGGTGGTAAGCAACTCTAAG 1816

Fig. 5C



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TCTGTATTGGTATTGGTCATTCTCAGTGGAAATCCCTTAGGCCCTACTAGTGTTTCCCCTACCTGCATATTGGTTTC 1895
ATGTTTATATTCACTGTTACTATCTCTGTGTAAATTAAATTGTTCTATCAAAAAAAAGGGC 1974
GGCCGC 1980

Fig. 5D



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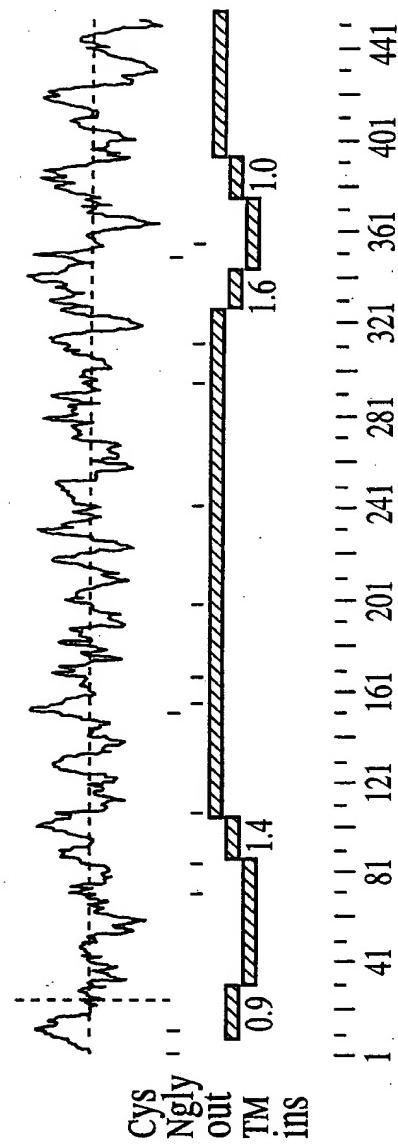


Fig. 5E



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10	20	30	40	50	60
286 MCTKT-IPVILWGCFL-LWNLYVSSSSQTIYPGIKARITQRALDYGVQAGMCKMIEQMLIKEKKLPPDLSGSESL					
:	:	:	:	:	:
BPI MARGPCNAPRWVSLMVVLVAIGTAVTAANPGVVVRISQKGGLDYASQQGTAALQKELKRIKIPDYS--DSF					
10	20	30	40	50	60
70	80	90	100	110	120
286 EFLIKVVDYVNYYNFSNIKISAFSFPNSTS LA FV PGVG IKAL TNHGT ANI ST DWGFESPLFVLYNSFAEPME--					
:	:	:	:	:	:
BPI KIKHLGKGHYSFYSMIDIREFQLPSSQIISMVPNVGLKF SISNANIKISGKWKAOQKRFLKMSGNFDLSIEGM					
70	80	90	100	110	120
10	20	30	40	50	60
140	150	160	170	180	190
286 -----KPI-----					
:	:	:	:	:	:
BPI SISADLKLGNSNPTSGKPTITCSSSSHINSVHVHSKS SKV GMLI QLFHKKIESALRNKMNSQVCEKVNTNS					
140	150	160	170	180	190
150	160	170	180	190	200
160	170	180	190	200	210
286 VKA-LNANLISTLEVLT KIDNYTLLDYSLISSPEITENYLDLN LKG VFYPLENLTDPPFSPVPPFVL PERSN					
:	:	:	:	:	:
BPI VSSKLQPYFQTLPVMTKIDS VAGINYGLVAPPATTAE TLDVQMKG EFYSENHHNPPPFA APPVMEFPAAHD					
210	220	230	240	250	260
220	230	240	250	260	270

Fig. 5F



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230 240 250 260 270 280 290
286 SMLYIGIAEYFFKSASFAHFTAGVFNLTLSTEEISNH--FVQNSQGILGNVLSSRAEIYIYLSQLP
::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
BPI RMVYLGSLSDYFFNTAGLVYQEAGVLUKMTLRRDDMIPKESKFRLTTKFFGTFLPEVAKKFPMVKIQIHVSA
280 290 300 310 320 330 340

300 310 320 330 340 350 360
286 TEPPIIINLQPGNFTILDIPASIMMLTQPKNSTVETIVSMSDFVAASTSVGLVILGQLRVCSSLNRFRLLALPE
::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
BPI STPPHLSVQOPTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELKHH
350 360 370 380 390 400 410

370 380 390 400 410 420 430
286 SNRSNIEVLRFENILSSILHFGVPLANAKLQQGFPLPNPHKELFVNDSIEVLEGFLLISTDLKYETSSK
::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
BPI SNIGPFPVELLQDIMNYIVPILVLPRVNEKLIQKGFPPLPTPARVQLYNVVLQPHQNFLIFGADVYK----
420 430 440 450 460 470 480

440 450
286 QQPSFHVWEGLNLIISRQWRGKSAP

BPI -----

Fig. 5G



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Fig. 5H



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51
Eig.



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GTCGACCCACGGCGTCCGGGAATTGCAGCAGAAAATATGTGAAGAGTTTAAACCCACAAATTCTTACTTTAGA
 ATTAGTTACATTGGCAGGAAAATAATGCAGATGTTGGACC ATG TTG GAA ACC TTG TCA AGA CAG 79
 W I V S H R M E M W L L I L V A Y M F Q 8
 TGG ATT GTC TCA CAC AGA ATG GAA ATG TGG CTT CTG ATT CTG GTG GCG TAT ATG TTC CAG 149
 R N V N S V H M P T K A V D P E A F M N 28
 AGA AAT GTG AAT TCA GTA CAT ATG CCA ACT AAA GCT GTG GAC CCA GAA GCA TTC ATG AAT 209
 I S E I I Q H Q G Y P C E E Y E V A T E 48
 ATT AGT GAA ATC ATC CAA CAT CAA GGC TAT CCC TGT GAG GAA TAT GAA GTC GCA ACT GAA 269
 D G Y I L S V N R I P R G L V Q P K K T 68
 GAT GGG TAT ATC CTT TCT GTT AAC AGG ATT CCT CGA GGC CTA GTG CAA CCT AAG AAG ACA 329
 D G Y I L S V N R I P R G L V Q P K K T 88
 GAT GGG TAT ATC CTT TCT GTT AAC AGG ATT CCT CGA GGC CTA GTG CAA CCT AAG AAG ACA 389
 G S R P V V L L Q H G L V G G A S N W I 108
 GGT TCC AGG CCT GTG GTG TTA CTG CAG CAT GGC CTA GTT GGA GGT GCT AGC AAC TGG ATT 449
 S N L P N N S L G F I L A D A G F D V W 128
 TCC AAC CTG CCC AAC AAT AGC CTG GGC TTC ATT CTG GCA GAT GCT GGT TTT GAC GTG TGG 509
 M G N S R G N A W S R K H K T L S I D Q 148
 ATG GGG AAC AGC AGG GGA AAC GCC TGG TCT CGA AAA CAC AAG ACA CTC TCC ATA GAC CAA 569

Fig. 6A



D	E	F	W	A	F	S	Y	D	E	M	A	R	F	D	L	P	A	V	I
GAT	GAG	TTC	TGG	GCT	TTC	AGT	TAT	GAT	GAG	ATG	GCT	AGG	TTT	GAC	CTT	CCT	GCA	GTG	ATA
N	F	I	L	Q	K	T	G	Q	E	K	I	Y	Y	V	G	Y	S	Q	G
AAC	TTT	ATT	TTG	CAG	AAA	ACG	GGC	CAG	GAA	AAG	ATC	TAT	TAT	GTC	GGC	TAT	TCA	CAG	GGC
T	T	M	G	F	I	A	F	S	T	M	P	E	L	A	Q	K	I	K	M
ACC	ACC	ATG	GGC	TTT	ATT	GCA	TTT	TCC	ACC	ATG	CCA	GAG	CTG	GCT	CAG	AAA	ATC	AAA	ATG
Y	F	A	L	A	P	I	A	T	V	K	H	A	K	S	P	G	T	K	F
TAT	TTT	GCT	TTA	GCA	CCC	ATA	GCC	ACT	GTT	AAG	CAT	GCA	AAA	AGC	CCC	GGG	ACC	AAA	TTT
L	L	L	P	D	M	M	I	K	G	L	F	G	K	E	F	L	Y	Q	228
TTG	TTG	CTG	CCA	GAT	ATG	ATG	ATC	AAG	GGA	TTG	TTT	GGC	AAA	AAA	GAA	TTT	CTG	TAT	CAG
T	R	F	L	R	Q	L	V	I	Y	L	C	G	Q	V	I	L	D	Q	I
ACC	AGA	TTT	CTC	AGA	CAA	CTT	GTT	ATT	TAC	CTT	TGT	GGC	CAG	GTG	ATT	CTT	GAT	CAG	ATT
C	S	N	I	M	L	L	G	G	F	N	T	N	N	M	N	M	S	R	288
TGT	AGT	AAT	ATC	ATG	TTA	CTT	CTG	GGT	GGA	TTC	AAC	ACC	AAC	AAT	ATG	AAC	ATG	AGC	CGA
A	S	V	Y	A	A	H	T	L	A	G	T	S	V	Q	N	I	L	H	W
GCA	AGT	GTA	TAT	GCT	GCC	CAC	ACT	CTT	GCT	GGA	ACA	TCT	GTG	CAA	AAT	ATT	CTA	CAC	TGG
S	Q	A	V	N	S	G	E	L	R	A	F	D	W	G	S	E	T	K	N
AGC	CAG	GCA	GTG	AAT	TCT	GGT	GAA	CTC	CGG	GCA	TTT	GAC	TGG	GGG	AGT	GAG	ACC	AAA	AAT

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Fig. 6B



L E K C N Q P T P V R Y R V R D M T V P 348
 CTG GAA AAA TGC AAT CAG CCA ACT CCT GTA AGG TAC AGA GTC AGA GAT ATG ACG GTC CCT 1169

T A M W T G G Q D W L S N P E D V K M L 368
 ACA GCA ATG TGG ACA CGA GGT CAG GAC TGG CTT TCA AAT CCA GAA GAC GTG AAA ATG CTG 1229

L S E V T N L I Y H K N I P E W A H V D 388
 CTC TCT GAG GTG ACC AAC CTC ATC TAC CAT AAG AAT ATT CCT GAA TGG GCT CAC GTG GAT 1289

F I W G L D A P H R M Y N E I I H L M Q 408
 TTC ATC TGG GGT TTG GAT GCT CCT CAC CGT ATG TAC AAT GAA ATC ATC CAT CTG ATG CAG 1349

Q E E T N L S Q G R C E A V L * 424
 CAG GAG ACC AAC CTT TCC CAG GGA CGG TGT GAG GCC GTA TTG TGA 1397

AGCATCTGACACTGACCGATCTTAGGACAACCTCCTGAGGGATGGGGCTAGGACCCATGAAGGCCAGAAATTACGGAGAGCA 1476
 GAGACCTAGTATACTTTCAAGATTCCCTGCACCTGGCACTTACATTCCGACACTACATTACATTTCTGTAAA 1555
 TTAAAGTACTTATTAGGTAATAAGGGTTTGTATGCTATTATATATTCTACCATCTACCATCTACATTTCTGTAAA 1634
 AGCCAGAAAATCTAGACATCTCTATCATTCAAGTAAATCTCTAAACACCTATTGTTCTATAAGCCAT 1713
 ATTTTGGAGCACTAAAGTAAAATGGCAAAATTGGACAGATATTGAGGTCTGGAGTCTGTGGATTATTGTTGACTTTGA 1792
 CAAATAAGCTAGACATTTCACCTTGCCACAGAGACATAACACTACCTCAGTAAAGCATTTAGGTATGGATGTTATAGTTGACAA 1871
 CAACACAAAAATCAGTGTACAGTATGGATGAAATCTAGTAAAGCATTCAGAATAAGGCCAAGTTTATAGTTGCA 1950
 TCTCAGGGAAAGAAAATTTTATAGGATGTTATGAGTTCTCCAAATAATGCATTCTGCATTACATAAAAAA 2029
 AAAAGGGCGCCGC 2044

Fig. 6C



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10	20	30	40	50	60	70
294 MLETLSROWIVSHRMEMWLLILVAYMFQRNVNSVHMPPTKAVDPEAMNISEIIQHQGPCEEYEVATEDG						
:	⋮	⋮	⋮	⋮	⋮	⋮
HLP M-----WLL---LTMASLISVLGTTHGLFGKLH-----PGSPEVTMNIQSQMITYWGYPNEEYEVVTEDG						
10	20	30	40	50	60	70
80	90	100	110	120	130	140
294 YILSVNRIPRGLVQPKKTGSRPVVILLQHGLVGASNWIISLNPNNSLGFILADAGEDFVWMGNSRGNAWSRK						
⋮	⋮	⋮	⋮	⋮	⋮	⋮
HLP YILEVNRIPYGKKNSGNTGQRPVVFLOQHGLLASATNWISLNPNNSLAFILEADAGYDWLGNSRGNWTARR						
60	70	80	90	100	110	120
150	160	170	180	190	200	210
294 HKTLSIDQDEFWAEFSYDEMARFDLPAVINFILEQKGTQEKEIYYVGYSQGTTMGFIAFSTMPELAQKIKMYF						
⋮	⋮	⋮	⋮	⋮	⋮	⋮
HLP NLYYSPDSVEFWAEFSFDEMAYKDLPATIDEIVKKTGQKQLHYVGHSQGTTIGFIAFSTNPSLAKRIKTFY						
130	140	150	160	170	180	190
220	230	240	250	260	270	
294 ALAPIATVKHAKSPGTKFLLLPDMMIKGLFGKKEFLYQTRFLRQ-LVIYLCCQVILDQICSNIMLLGGF						
⋮	⋮	⋮	⋮	⋮	⋮	⋮
HLP ALAPVATVKYTKSLINKLRFVPQSLFKIFGDKIF-YPHNFFDQFLATEVCSCREMLNLLCSNALFIICGF						
200	210	220	230	240	250	260

Fig. 6D



280 290 290 300 310 320 330 340
294 NTNNMMSRASVYAAHTLAGTSVQNLHWSQAVNSGELRAFDWGSETKNLEKCNQOPTPVRYRVRDMTVPT
... :
HLP DSKNFNTSRLDVYILSHNPAGTSVQNMFHWTQAVKSGKFQAYDWGSPPVQNRMHYDQSQQPPYYNVNTAMNVPI
270 280 280 290 300 310 320 330

350 360 370 380 390 400 410
294 AMWTGGQDWLWSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIFIWGLDAPHMYNEIIHLMQQEETNLSQGRC
... :
HLP AVWNNGKDLIADPQDVGLLPKLPNLIYHKEIPFYNHLDIFIWAMDAPQEJVYNDIVSMISEDKK-----
340 350 360 370 380 390 390

420
294 EAVL
HLP -----

Fig. 6E



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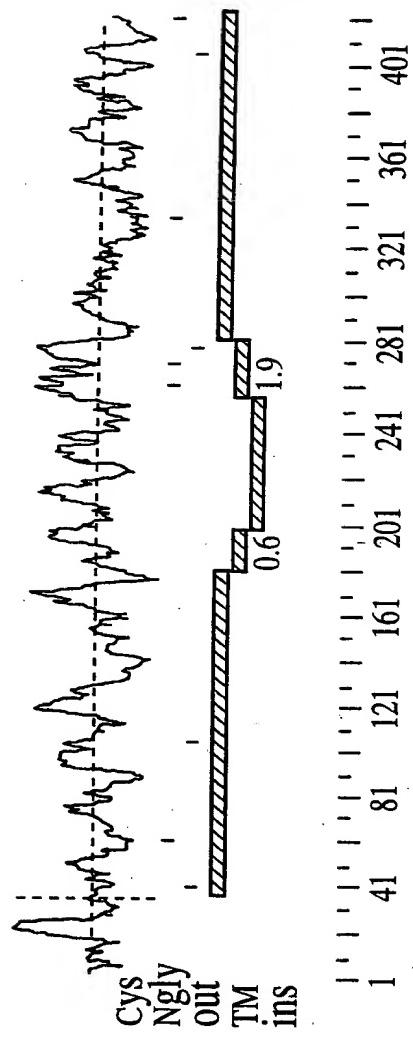


Fig. 6F



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10 20 30 40 50 60
MLETLSRQWIVSHRMEMWLILVAYMFQRNVNSVHMPTK--AVDPEAFMNISEIIQHQGYPCEEYEVATE
:
: : : : :
LAL M-----KMRFLGLVVCLVLWPLHSEGGKLTAVDPETNMNVSEIISYWGFPSEEYLVETE
10 20 30 40 50

70 80 90 100 110 120 130
DGYILSVNRIPRGILVQPKRTGSRPVVLQQHGLVGGASNWISSLPNNSLRGNNAWS
:
: : : : :
LAL DGYILCLNRIPHGRKNHSDKGPKPVVFQHGLLADSSNWVTNLANS SLGFILADAGFDVWMGN SRGNTWS
60 70 80 90 100 110 120

140 150 160 170 180 190 200
RKHKTLSIDQDEFWAFSYDEMARFDLPAVINFILEQKTGQEKEIYYVGYSQGTTMGFIAFSTMPELAQKIKM
:
: : : : :
LAL RKHKTLSVSQDEFWAFSYDEMAKYDLPASINFILNKTGQEQQVYYVGHQSQGTTIGFIAFSQIPELAKRIKM
130 140 150 160 170 180 190

210 220 230 240 250 260 270
YFALAPIATVKHAKSPGTKFILLPDMMIKGLFGKKFLYQTRFLRQLVIYLCGVVILDQICSNIMLLGG
:
: : : : :
LAL FFALGPVASVAFCTSPMAKLGRILPQSAFLKWLGFDTVILKELCGNLCLFLICG
200 210 220 230 240 250 260

Fig. 6G



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280 290 300 310 320 330 340
294 FNTNNNMRSRASVYAAHTLAGTSVQNIHLHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRVYRVRDMTVP
::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
LAL FNERNLNMSRVDVYTTHSPAGTSVQNIHLHWSQAVKFQKFAQEDWGSSAKNYFHYNQSYPPTYNVKDMLVP
270 280 290 300 310 320 330

350 360 370 380 390 400 410
294 TAMWTGGQDWLSNPEDVKMILLSEVTNLIYHKNIPEMAHVDFIWLDAAPHRYNEIIHLMQQEETTNLSQGR
::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
LAL TAWWSSGGHDWLADVYDVNILLTQITNLVFHESIPEWEHLDEFIWLDAFWRLYNNKIINLMRKYQ-----
340 350 360 370 380 390

420
294 CEAVL
LAL -----

Fig. 6H



GTCGACCCACGGGTCCACGGCGAGGGCTCCCCGGGGCAGCATTTGCCACCCCTGCACCAAG ATG GCT 75
 T L G H T F P F Y A G P K P T F P M D T 22
 ACT TTG GGA CAC ACA TTC CCC TCC TAT GCT GGC CCC AAG CCA ACC TTC CCG ATG GAC ACC 135

T L A S I I M I F L T A L A T F I V I L 42
 ACT TTG GCC AGC ATC ATC ATG ATC TTT CTG ACT GCA CTG GCC ACG TTC ATC GTC ATC CTG 195

P G I R G K T R L F W L R V V T S L F 62
 CCT GGC ATT CGG GGA AAG ACC AGG CTG TTC TGG CTG CTT CGG GTG ACC AGC TTA TTC 255

I G A A I L A V N F S S E W S V G Q V S 82
 ATC GGG GCT GCA ATC ATC CTG GCT GTG AAT TTC AGT TCT GAG TGG TCT GTG GGC CAG GTC AGC 315

T N T S Y K A F S S E W I S A D I G L Q 102
 ACC AAC ACA TCA TAC AAG GCC TTC AGT TCT GAG TGG ATC AGC GCT GAT ATT GGG CTG CAG 375

V G L G V N I T L T G T P V Q Q L N E 122
 GTC GGG CTG GGT GGA GTC AAC ATC ACA CTC ACC GGG ACC CCC GTG CAG CAG CTG AAT GAG 435

T I N Y N E E F T W R L G E N Y A E E C 142
 ACC ATC AAT TAC AAC GAG GAG TTC ACC TGG CGC CTG GGT GAG AAC TAT GCT GAG GAG TGT 495

A K A L E K G L P D P V L Y L A E K F T 162
 GCA AAG GCT CTG GAG AAG GGG CTG CCA GAC CCT GTG TTG TAC CTA GCT GAG AAG TTC ACT 555

Fig. 7A



P	R	S	P	C	G	L	Y	R	Q	Y	R	L	A	G	H	Y	T	S	A	182
CCA	AGA	AGC	CCA	TGT	GGC	CTA	TAC	CGC	CAG	TAC	CGC	CTG	GCG	GGA	CAC	TAC	ACC	TCA	GCC	615
M	L	W	V	A	F	L	C	W	L	L	A	N	V	M	L	S	M	P	V	202
ATG	CTA	TGG	GTG	GCA	TTC	CTC	TGC	TGG	CTG	CTG	GCC	AAT	GTG	ATG	CTC	TCC	ATG	CCT	GTG	675
L	V	Y	G	G	Y	M	L	L	A	T	G	I	F	Q	L	L	A	L	L	222
CTG	GTA	TAT	GGT	GGC	TAC	ATG	CTA	TTG	GCC	ACG	GGC	ATC	TTC	CAG	CTG	TTG	GCT	CTG	CTC	735
F	F	S	M	A	T	S	L	T	S	P	C	P	L	H	L	G	A	S	V	242
TTC	TTC	TCC	ATG	GCC	ACA	TCA	CAC	TCA	CCC	TGT	CCC	CTG	CAC	CTG	GGC	GCT	TCT	GTG	795	
L	H	T	H	G	P	A	F	W	I	T	L	T	T	G	L	L	C	V	262	
CTG	CAT	ACT	CAC	CAT	GGG	CCT	GCC	TTC	TGG	ATC	ACA	TTG	ACC	ACA	GGA	CTG	TGT	GTG	855	
L	L	G	L	A	M	A	V	A	H	R	M	Q	P	H	R	L	K	A	F	282
CTG	CTG	GGC	CTG	GCT	ATG	GCG	GTG	GCC	CAC	AGG	ATG	CAG	CCT	CAC	AGG	CTG	AAG	GCT	TTC	915
F	N	Q	S	V	D	E	D	P	M	L	E	W	S	P	E	E	G	G	L	302
TTC	AAC	CAG	AGT	GTG	GAT	GAA	GAC	CCC	ATG	CTG	GAG	TGG	AGT	CCT	GAG	GAA	GGT	GGA	CTC	975
L	S	P	R	Y	R	S	M	A	D	S	P	K	S	Q	D	I	P	L	S	322
CTG	AGC	CCC	CGC	TAC	CGG	TCC	ATG	GCT	GAC	AGT	CCC	AAG	TCC	CAG	GAC	ATT	CCC	CTG	TCA	1035
E	A	S	S	T	K	A	Y	C	K	E	A	H	P	K	D	P	D	C	A	342
GAG	GCT	TCC	TCC	ACC	AAG	GCA	TAC	TGT	AAG	GAG	GCA	CAC	CCC	AAA	GAT	CCT	GAT	TGT	GCT	1095

Fig. 7B



L *
TTA TAA

344
1101

CATTCTCCCGTGGAGGCCACCTGGACTTCCAGTCACCGGACTTGGCTCAAACCTCATTGGCCCCATAAAACCAGGAACTG 1180
CCCTCAAGGGGGCTTACAGACACCCAGAACAACTACAGACGGAGTAGAAAAAGGGCTCTATATACTGATGTT 1259
AAAAAAACAAAACAAAAGCCCTAAGGGACTGAAGAGATGCTGGGCCTGTCCATAAGGCCATTAAGGCTGTTGCCATGATAAG 1338
GCCAAGCAGGGCTAGCTTATCTGCACAGCAACCCAGGCCTTCCGTGCTGCCTCTCAAGATGCTTCAAGATGCTTCAACTGAA 1417
AACCTAACCTCACCCCCATAACACGGCAGGGTGGGGTTACATATGATTCTCCTATGTTTCCCTCATCCCTCGGCA 1496
CCTCTGTTTCTGGTTCTTCTGGCTTCTTGTCTCCCTTACTCTCCAGCTTGTGGCCCTTTGGTACAATGAA 1575
AGACAGGCACTGGAAAGGGAAACCAAAACTTCTCATCCTAGGTCTAACATTAACTAACATTGCAACTATGCCACATTCTCTTGA 1654
GCTTCAGTTCCCAATTGCTACATAAGATTGCAAGACTTGCCAAGAATCTGGATTATCTTCTATGCCCTTGTGCTGA 1733
CACCTACCTTGGCCTCAAACACCCTCACAAAGAACCCAGGTGGGAAGTTAGGGAACTCAACTCCAAAACGCTATTCCCT 1812
TCCCACCCCACTCAGCTGGCTAGCTGAGTGGCATCCAGGACGGGGAGTGGGTGACCTGCCTCATCACTGCCACCTAA 1891
CGTCCCCCTGGGGTGGTTCAAGAAAGATGCTAGGCTAGGGCCCTTCCGGCCTCACTAGGGGGCTCAGTGGGTGTTCTG 1970
TGGAGTCGACGCCAGAAATCAAGTTACAGGACTGGGAGGTGTACTAGGGTGTCTCCAGCCCCAGGGAAAGCTCATGAA 2049
GGACGTGGCACCCGGCGGGAAAGCCATGAAAATTAAATGGAAAAACAGTTTAAACAGTTTAAATGGAAAA 2128
GCCGC 2133

Fig. 7C



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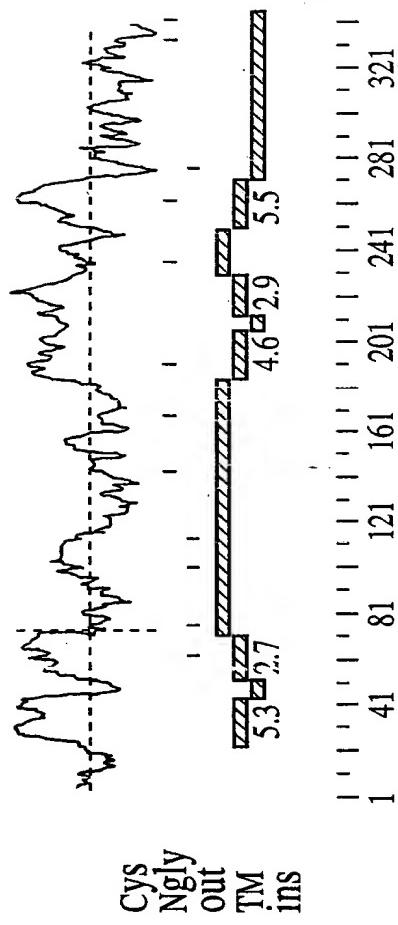


Fig. 7D



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10 20 30 40 50 60 70
296 MATLGHTEPFYAGPKPTFPMDTTIASIIMIFLTALATFIVILPGIRGKTRLFWLLRVVTSLFIGAAILLAV
: : :
CRP M-RIAH----ASSRGNI-----SIFSVEFLIAYILILPGVVR-RKRVVTTVTVYVMLAVGGALLAS
10 20 30 40 50

80 90 100 110 120 130
296 NFSSEWSVGQVSTNTSYRAFSSEWISADIGLQVGLGGVNITL-----TGTTPVQQQLNETIN--YNEEFTW
: : :
CRP LIYPCWASGSQMIYTQFRGHSNERILAKIGVEIGLOQKVNVTLKFERILSSNDVLPGSDMTELYYNEGEFDI
60 70 80 90 100 110 120

140 150 160 170 180 190 200
296 RLGENYAEECAKALEKGGLPDGVLYLAEKFT-PRSPCGLYRQYRLAGHYTSAMLWWAFLCWLLANV-MLSM
: : :
CRP SGISSMAEAHHGLENGLPYPMILSVLEYFSLNQDSFDWGRHYRVAGHYTHAAIWFAFACWCLS VVILFL
130 140 150 160 170 180 190

210 220 230 240 250 260
296 PVLVYGGYMLLATGIFQLLALLFFSMSATSLTSPCPLH---GASVLHHTHGPAT---WITLTTGLLCWL
: : :
CRP PHNAYKS--ILATGISCLIACLVYL---LLSPCELRIAFTGENFERVDLTATESFCCFYLIFAIIGILCWL
200 210 220 230 240 250 260

Fig. 7E



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270 280 290 300 310 320
296 LGIAMAVERHMQPHRLKAFNQSVDDEDPMLEW-----SPEEGGLLSSPRY--RSMADSPKSQDIPPLEAS
::: :: .
CRP CGLGLGICHEHWRIYTTLSTFLDASLDEHVGPKWKKLPTGGPALQGVQIIGAYGTNTNSRDKNDISSLKTA
270 280 290 300 310 320 330

330 340
296 STKAY-----CK-----EAHPKDPD-----CA---L
::: :: .
CRP GSSGFQSRTSTCQSSASSASLRSQSSIETVHDEAELERTHVFQEPCSSSSST
340 350 360 370 380

Fig. 7F